

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 103654

TO: Karen A Lacourciere

Location: CM1/11D09&11E12

Art Unit: 1635

Saturday, September 13, 2003

Case Serial Number: 09/763590

From: Mary Jane Ruhl

Location: Biotech-Chem Library

CM1-6A06

Phone: 605-1155

maryjane.ruhl@uspto.gov

Search Notes

Examiner Lacourciere,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl Technical Information Specialist STIC CM-1, Rm. 6-A-06 605-1155



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/done_libs_"Addult 5;0 7/94"
//done_libs_"Addult 5;0 7/94"
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//done_libs_"Addult 5;0 7/94"
//done_"Vector: Lambda ZAP-II XR.; Site_I: ECOR I; Site_2: Xhol I: Several hundred addult Schistosma japonicum (Anhui y. P. R. China, strain), of mixed sex, were perfused from the mesenteries of experimentally infected mice and rabbits at the Queensland Institute of Medical Research, Brisbane, Australia (QIMR), and stored for several months in liquid nitrogen. Subsequently, mRRN was isolated at the QIMR from lysates of these worms by oligo dr chromatography, using a kit from Pharmacia. The mRNA was then shipped to Clontech, Palo Alto, CA, USA, who constructed a cDNA library. First strand synthesis was primed with an oligo-dr-Xhol-primer and synthesis was accomplished with RNAse H and T4 DNA polymerase. The double stranded cDNA was ligated to ECORI linkers, digested with ECORI and Xhol, and ligated into the phagemid vector lambda ZAP II XR. After construction of this directional library by Clontech, it was returned to the QUMR. During analysis of the library at the QIMR, we have the QUMR. During analysis of the library at the QIMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schistosoma japonicum
Schistosoma japonicum
Schistosoma japonicum
Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosoma.

( pases 1 to 543)
Hu,W., Yan,Q., Shen,D., Liu,F., Xu,X., Zhu,Z., Zhang,X., Wang,J.,
Sun,J., Xu,X., Wang,Z., Zeng,L., Rong,Y., Wu,X., Qu,J., Xu,Z.,
Huang,J., Ma,Y., Wang,S., Wang,Z., Xue,C., Feng,Z., Chen,Z. and Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU712126 543 bp mRNA linear EST 12-FEB-2003 SJAAAWA07 Adult Sjc 7/94 Schistosoma japonicum cDNA, mRNA sequence.
                                                                                                                                                                1 ACCGUUGGUUUCCGUAGUGUAAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
S51 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.
                                                                     Gaps
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                                                                  0;
Query Match

45.0%; Score 63.4; DB 29; Length 617;

Best Local Similarity 68.5%; Pred. No. 4.7e-10;

Matches 50; Conservative 17; Mismatches 6; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Chinese (Anhui) strain"
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BU712126
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have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma

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5 UUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCG 64
                                                                                                                             0; Gaps
                                                                                           44.4%; Score 62.6; DB 13; Length 543; 69.6%; Pred. No. 8.4e-10; Live 17; Mismatches 4; Indels 0;
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              Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Ciona intestinalis genomic fragment, clone 3E10, genomic survey
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BP 191 91006 EVRY cedex .- FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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Clark, V.H., Leitgeb, S., Charlton, J., Tweedie, S., Simmen, M.W. and
                                                                                                                                                                                                                                                                                                                                                                     8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-FEB-1998) ICMB, University of Edinburgh, King's Bulidings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact: VGLARK@SIVO.bio.ed.ac.uk
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                     /note="Genoscope sequence ID : C0AG219CH01SP1~end
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                                                                                                                                                                                                                                                                                                    45.1%; Score 63.6; DB 29; Length 206; 74.2%; Pred. No. 3.4e-10; rative 16; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                         12 others
                                                                                                                                 /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Science 283 (5405), 1164-1167 (1999)
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GGSS; games survey sequence.
Ciona intestinalis
Ciona intestinalis
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Sequence analysis of transposable elements in the sea squirt, Ciona intestinalis
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Clark,V.H., Leitgeb,S., Charlton,J., Tweedie,S., Simmen,M.W. and
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Ciona intestinalis genomic fragment, clone 11G6, genomic survey
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Nonmethylated transposable elements and methylated genes in a
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VCLARKGsrvO. bio. set.uk
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                                                                                                                                                                                 Length 590;
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/organism="Ciona intestinalis"
/mol_type="genomic_DNA"
/db_xref="taxon:7719"
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/organism="Ciona intestinalis"
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Science 283 (5405), 1164-1167 (1999)
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/db_xref="taxon:7719"
/clone="11G6"
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Ciona intestinalis
Ciona intestinalis
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/dev_stage="adult"
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113 c 126 q
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AJZ26216.1 GI:2949677
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                                                                                                                                                                                                                                                                               Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.ons.fr
                                                                                                                                                                                                                                                                                                                        Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
6000me Res. 10 (7), 939-949 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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BX297643 AGENAE Rainbow trout multi-tissues subtracted library (tcay) Oncorhynchus mykiss cDNA clone tcay0002b.i.04 5prim, mRNA
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/note="Genoscope sequence ID : Claa0072D04C1-end : T7"
1 202 c 217 g 347 t 19 others
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Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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                                                          Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.
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Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Construction and primary characterization of noi
libraries in rainbow trout, Oncorhynchus mykiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Oncorhynchus mykiss
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                                                                                                                                                                                                           /clone_itcoy/00255.1.04"
//tissue_tropy/0255.1.04"
/itssue_trope="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
//dev_stage="from embryos to adults"
/lab_host="pH108"
/lab_host="pH108"
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 219P01 of library G from Tetraodon nigroviridis, genomic survey
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Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Perconorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          library (tcay) "
//note="vector: PTT3D-pac; Clone distribution : AGENAE
Resource centre. Francois PIUMI,
Francois.Plumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE"

116 c 145 g 153 t
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                                                                                                                         /organism="Oncorhynchus mykiss"
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                                                                                                                                                    /mol_type="mRNA" /db_xref="taxon:8022"
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Tetraodon nigroviridis
Tetraodon nigroviridis
                                                         Location/Qualifiers
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
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                                                                                                                                                                           library availability, please contact Pieter de Jong
pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea of Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
DooR: Site_2: ECORI; Female C57BL/6J mouse kithey and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus Subrayotas (Craniata; Vertebrata; Euteleostomi; Mammalia; Metheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 695)
1 (bases 1 to 695)
2 (bases 1 to 695)
3 (bases 1 to 695)
4 (bases 1 to 695)
8 (bases 1 to 695)
8 (bases 1 to 695)
9 (bases 1 to 695)
1 (bases 1 to 695)
2 (bases 1 to 695)
3 (bases 1 to 695)
4 (bases 1 to 695)
4 (bases 1 to 695)
5 (bases 1 to 695)
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2M0273K10F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished
                                                                                                                                               Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/69"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="RPC1-23-144M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ989726.1 GI:13860953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                           Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                   301 838 0200
301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 cc66GC 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 CCGGGC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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KEYWORDS
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AZ989726
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(http://www.pax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 (pblART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll xL10-Gold (Stratagene) cells and selected for amplcillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 01-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="E. coli strain XLI0-Gold, Tl-resistant, F-"

/clone_lib="Mouse lokb plasmid UGC2M library"

/note="vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodon nigroviridis genome survey sequence T7 end of clone 038H13 of library A from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.7%; Score 64.4; DB 28; Length 695; 74.2%; Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                               Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
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Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0273 row: K column: 10
Seg primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                                                                                                      High quality sequence stop: 695.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UGGC2M0273K10"
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Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL306891.1 GI:8208133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49; Conservative
                                                                                                                                                                                                                                          1. .695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 CCGGGC 73
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Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A2115558 23-MUS 232 bp DNA linear GSS 12-MAY-2000 RPCI-23-16D17.TV RPCI-23 Mus musculus genomic clone RPCI-23-16D17, genomic survey sequence.
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Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CHORI-240"
//clone_lib="CHORI-240"
//note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull ll Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
60 c '49 g dat 2 34 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.7%; Score 64.4; DB 29; Length 201; 74.2%; Pred. No. 1.8e-10; tive 16; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                       Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="breed: Hereford"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing Initiative)
Plate: 70 row: 0 column: 13
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="CH240_70013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="Blood"
                                                                                                                                                           Other_GSSs: CH240_70013.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                         Email: h-lewin@uiuc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AZ115558.1 GI:7776690
                                                                                                                                                                                      Contact: Harris Lewin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .201
                                                                                                           Genome Sequence
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                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 CCGGGC 44
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/clone_lib="RECI-23"
/clone_lib="RECI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note penomic DRA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
/noted DRA was cloned into the pBACe3.6 vector at the
/note sites. The ligation products were transformed into
/note penompetent cells (BRL Life Technologies). "
/note="DRA page 12"
/note="DRA page 12"
/note="DRA page 13"
/note="DRA page 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ288311 57-JUL-2000 FPCI-23-144M11.TJ RPCI-23 Mus musculus genomic clone RPCI-23-144M11
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                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.mac.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tab/bac_ends/mouse/bac_end_intro.html
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 574)
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Unpublished
Other_GSSS: RPCI-23-16D17.TJ
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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Other_GSSs: RPCI-23-144M11.TV
Contact: Shaying Shao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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/strain="C57BL/6J"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ288311.1 GI:9530097
                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
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Class: BAC ends.
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GSS 01-JUL-1998

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 390) Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                       AQ030852
HS_2182_B2_H05_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2182 Col=10 Row=P, genomic survey
                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="Plate=2182 Col=10 Row=P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
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Location/Qualifiers
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Plate: 2182 row: P column: 10
Class: BAC ends
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                                                                                                                                                                                       Homo sapiens (human)
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223 CCGGGCA 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: schaoetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availablilty, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
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                                                                                                                                                                                                           GSS 30-NOV-2001
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/clone_lib="CHORI-210 Segment 1"
/note="Vector: praRBAC2.1; Site_1: ECORI; Site_2: ECORI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by Pieter de Jong"
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                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Plate: 179 row: P column: 7
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                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_GSSS: CH230-179P7.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                           DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                           720 bp
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/clone="CH230-179P7"
                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
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                                                                                     64 GAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                       BH305888.1 GI:17218296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 720)
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Fax: 301 838 0208
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CHILD DNA linear GSS 12-JUN-2003 CHILD DNA linear GSS 12-JUN-2003 CHILD CHILD CHILD GENOMIC SURVEY SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
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Class: BAC ends.
Seq primer: T7
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RPCI-23-404J7.IV RPCI-23 Mus musculus genomic clone RPCI-23-404J7,
spennic survey sequence.
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_B. Levilas,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Frassz,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter deJong (pieter deJong mac, buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (lifo@resgen.com). BAC end page: http://www.tigr.org/tdb/bac.ends/mouse/bac_end_intro.html plate: 404 row: J column: 7
                                                          /Mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4080340"
/tissue_type="qlioblastoma"
/lab_host="DHIDB (TI phage resistant)"
/clone_lib="NIH_MGC_57"
/note="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
                                                                                                                                                                                                                    Sfil (ggcggctcggcc); Site_2: Sfil (ggcattatggcc), Double-stranded cDNA was prepared from cell line RNA. 5 and 3 dagbtor adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-0T(30)BN-3' (Where B = A, C, o G and N = A, C, G, O, T). Average insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)." 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 CCGGGGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGGT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 52.9%; Score 74.6; DB 10; Length 464; Best Local Similarity 62.3%; Pred. No. 1e-13; Matches 76; Conservative 16; Mismatches 30; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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                                         /organism="Homo sapiens"
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  Location/Qualifiers
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selected DNA was cloned into the pBAce3.6 vector at the EcoRI sites. The ligation products were transformed into DH108 electrocompetent cells (BRL Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was generated from the SP6 end of BAC 90F23. 90F23 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
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                                                                                                                                                                                                                      /lab_host="DHIOB"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and ECORI Methylase. Size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGU 61
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Actinoptersygii; Neoptersygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 767)
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/tissue_type="Testis"
/note="vector pindlogaAc-536"
144¢ 121 g 258 t
                                                       /organism="Mus musculus"
/mol_type="genomic DNA"
/krain="C57BL/69"
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/clone="RPCI-23-404J7"
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/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 767 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 TCGAAACCGGGCGGAAACAAGCA 135
Location/Qualifiers
1. .582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Danio rerio (zebrafish)
                                                                                                                                                                                                    /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 68.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54; Conservative
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BF244354 601862918
AZ062238 RPCI-23-4
BX132357 Danio rer
BH305888 CH230-179
                                                                         September 13, 2003, 09:43:56; Search time 1984.73 Seconds (without alignments) 1726.650 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                         US-09-763-590-2
141
1 accguugguuuccguagugu.....ggcacgucggaaacgguuuu 141
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                                                                                                                                                                                                                                           45562784
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                  22781392 segs, 12152238056 residues
                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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28 AZ062238
29 BX132357
28 BH305888
                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_gss_pln:*
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em_estom:*
em_gss_bum:*
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Maximum DB seq length: 2000000000
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em_estin: *
em_estip: *
em_estip: *
em_estip: *
em_btc: *
gb_esti: *
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Match Length DB
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582
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48.7
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Perfect score:
Sequence:
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68.6
66.8
66.2
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	~ ~	64.4 64.4	IO IO IO	695 1101 595	28	AZ989726 CNS04TSI RX297643	AZ9897. AL3068: RX2976.	26 2M0273K10 91 Tetraodon 13 BX297643
, , ,	c c c 113	63.6	45.1	2000	239	CNS0124U CI3E10	ALI738-	17 Tetraodon 30 Ciona int
		63.4 62.6 61.8	O ++ C	617 543 649	133	CIIIG6 BU712126 BX206800	AJ2262 BU7121: RX2068	16 Clona int 26 SJAAAWA07 30 Danio rer
Ŭ	0 17	61.6	ነጥ መ	418	188	AQ662870	AQ6628' BIT7115'	70 HS_5480_A
-	000	61.6	nm	802	53	CNS030W4	AL2564	77 Tetraodon
	270	61.6	ກຕເ	1046	5 6 6	CNS04YSZ	AL1/15 AL3133	31 Terracdon 38 Tetracdon
	77	61.6 61.6	നന	1101	53	CNS05MVY CNS05G97	AL3445 AL3360	79 Tetraodon 04 Tetraodon
	ი 24 ი 25	61.2 61.2	ന ന	467 834	9 13	AA489977 BW174938	AA48997 BW1749	7 aa98a04.s 38 BW174938
	NN	60.2 60.2	0 0	780	133	BW170857 BW302287	BW1708 BW3022	57 BW170857 37 BW302287
	388	000	(2)	777	57	BX176182	BX1761	82 Danio rer
	308	59.6	NN	1101	N 01	CNSUST4F CNS05AAR	AL3282 AL3282	84 Tetraodon
	me	59 8	4 0	1003	230	CNS051R1	AL3172	06 Tetraodon 93 Tetraodon
	333	28.	4	692	200	CNS023IT	AL1795	34 Tetraodon
	m r	58.6	-	981	600	CNS04CNF	AL2846	76 Tetraodon 29 Tetraodon
	36	58.6	⊣ ←	1002	2 6	CNS056ED	AL3232	30 Tetraodon
	c 37	58.4	-1-	610	53	DRIGEGS	AL7446	93 Danio rer
	n m	58.2	-1 -1	918	7 6	CNS0281F	AL1795	33 Tetraodon
	4.	85		338	13	BW166952	BW1669	52 BW166952
_	c 41	55 50 50 50 50 50 50 50 50 50 50 50 50 5	-1 -1	363	13 28	BW296387 BH063051	BH0630	BWZ9538 RPCI-24
	4.3	·	0	935	29	CNS 04 5M0	AL2755	53 Tetraodon
	44 45	56.8 55.8	00	819 936	29	BX232148 CC142986	BX2321 CC1429	48 Danio rer 86 NDL.37021
						ALIGNMENT	St	
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m ឯc	BF244354 LOCUS DEFINITION	BF24	14354 362918F1 NI	DEM HIN	ιn	464 bp n 7 Homo sapiens	mRNA linear EST 14 ens cDNA clone IMAGE:40803	T 14-NOV-2000 080340 5',
,		mRN	sednen	ce.	ì			
₹ \ ~	ACCESSION VERSION	BF2	14354 14354.1	GI:111	582	72		
14.0	KEYWORDS	EST	2 2 2 2	4				
<i>ν</i>	OURCE		sapien Sapien	s (numan) s	an)			•
			Eukaryota; Me Mammalia; Eut	Metazoa Jutheria	ая; О.С.	ordata; imates;	Craniata; Vertebrata; Eu Catarrhini; Hominidae; H	<pre>Euteleostomi; ; Homo.</pre>
ρκ	EFERENCE		(bases 1	1 to 464)	4)	n i b		
	TITLE TOTRNAL	Nati Nati	Nin-Mac nttp://myc.nci National Institutes of Unpublished	p://mg stitut	es o	f Health, M	, Mammalian Gene Collection	on (MGC)
Ō	COMMENT	Cont	act: Ro	bert S	tran	sberg, Ph.D		
		Emai	il: cgap	bs-rem uremen	ail. t: A	<pre>Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC</pre>		
		ପ୍ରି ପ୍ରି	MA Libra	ry Pre	para	tion: CLONE: by: The I.1	CLONETECH Laboratories, Inc. The I.M.A.G.E. Consortium (LLNL)	L'NL)
		DNG	Sequen	cing b	н Х.:	ncyte Genom.	ics, Inc.	04 200
		four	found through the I	gh the	. W.	A.G.E. Con:	M/LLNL	200
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High quality sequence stop: 142.

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SEQUENCE CHARACTERISTICS:
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TOPOLOGY: lin
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22.4%; Score 31.6; DB 3; Length 702;
Best Local Similarity 47.1%; Pred. No. 0.04;
Matches 33; Conservative 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Vorshavsky, Alexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSES: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: TWO Militia Drive
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILLING DATE: 24-DBC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF/5-30306/A/CGC1976
                   CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
CONWTK: USA
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: #20
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Medgs, J. Timchy
REGISTRATION NUMBER: 38.241
REFERENCE/DOCKET NUMBER: PF/5-30:
TELECOMMONICATION INFORMATION:
TELEPHONE: 919-541-8687
INFORMATION FOR SEQ ID NO: 947:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: PAG1586RP
US-08-998-416-947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 GAAACCGGGC 73
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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5 UUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCG 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.7%; Score 30.6; DB 1; Length 4887; Best Local Similarity 46.4%; Pred. No. 0.19; Matches 32; Conservative 13; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Tobias, John W.
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/005,002C FILING DATE: 15-JAN-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/789,915 FILING DATE: 08-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-5091AAZ
                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REPERROKEA/FOOKET UNBER: MIT-5091AA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-005-002C-7/c
; Sequence 7, Application US/08005002C
; Patent No. 5494818
; GENERAL INFORMATION:
                                                                                                                                                                                                   TELECORDON: 617-801 CT TELEPHONE: 617-801 CT TELEPHONE: 617-861-9540
| INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 4887 base pairs TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 207-363-0558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7:
                                           APPLICATION NUMBER: US
FILING DATE: 19911108
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207-363-0528
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P.O. Box 999
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: 1278..4013
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KET: MISC_feature
LOCATION: (12001)..(135000)
OTHER INPORMATION: n=a or c or g or t
NAME/KET: misc_feature
LOCATION: (13501)..(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (13501)..(165000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (13001)..(165000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (285001)..(300000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (300001)..(315000)
                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (195001)..(210000)
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LOCATION: (210001). (225000)
OTHER INPORATION: n=a or c or g or t
NAME/KEY: misc_feature
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LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (255001)..(270000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (270001)..(285000)
OTHER INFORMATION: n-a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (45001)...(60000)
OTHER INFORMATION: n=a.or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: na or c or g or t
NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (75001)..(90000)
OTHER INFORMATION: nea or c or g or t
NAME/KEY: misc_feature
LOCATION: (90001)..(105000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (225001)..(240000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (30001)..(45)
                                                                                                                                                             SEQ ID NO 1
LENGTH: 1230025
                                                                                                                                                                                                                                                                        FEATITE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 1, Application US/09198452A; Patent No. 6552294; GENERAL INFORMATION:
APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUÜCGAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.3%; Score 34.2; DB 4; Length 186; 52.1%; Pred. No. 0.0029; Live 11; Mismatches 23; Indels (
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
ATCHEGATION NUMBER: 60/08151
FILING DATE: July 2, 1997
ATCHET/ARBY INFORMATION:
NAME: ATINICALON PAMER: 40,489
REPERRINGE/DOCKET NUMBER: 40,489
REPERRINGE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...186
SEQUENCE DESCRIPTION: SEQ ID NO: 488:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                              US-09-107-532A-488/c
Sequence 488, Application US/09107532A
Patent No. 6583375
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 488: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
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Best Local Similarity 52.1%
Matches 37; Conservative
                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 CCGGGCACUAC 78
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                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-107-532A-488
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US-09-198-452A-1
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           RESULT 11
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US-08-270-076A-2
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                                                                                                   RESULT 10
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                                                                                                                                                                                                                   28 AGCGUGCUGGGCCCAUAACCCAGAGGUCGAUGGAUCGAAACCCCGGA--UCGUACCGCGG 85
                                                                                                                                       Gaps
                                                                                                                                       2;
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                                                                                            Query Match 29.2%; Score 41.2; DB 3; Length 146; Best Local Similarity 70.0%; Pred. No. 7.5e-06; Matches 70; Conservative 0; Mismatches 28; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCES: 25
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                         88 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCACG 127
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIOR APPLICATION DATR: Two
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886ember 10, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DCOKET NUMBER: 215/154
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5" Diskette, 1.44 Mb
MEDLUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFFWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CIT: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 67.4
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                   ; TOPOLOGY: linear
US-08-512-861A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Californi
COUNTRY: U.S.A.
ZIP: 90071
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US-08-512-861A-14
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14 GUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAACCGGGC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 123..124
OTHER INFORMATION: /product= "Sstil restriction site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: The BOC Group, Inc.
STREET: 100 Mountain Avenue, Murray Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/270,076A
CLASSIPICATION 1435
CLASSIPICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8923521.2
FILING DATE: 18-0CT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/597,687
FILING DATE: 16-0CT-1990
PRIOR APPLICATION NUMBER: US 07/597,687
FILING DATE: 16-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,286
FILING DATE: 04-AUG-1992
ATTORNEY/AGENT INFORMATION:
109 AAGGUCCGAAACGGCCACGUCGGAAA 134
                       126 AAGGUCCGAAACGGGCACACACAAAA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92H834-3
                                                                                                                                                                                                                                      APPLICANT: Sleep, Darrell
APPLICANT: Goody, Andrew R
APPLICANT: Vakeria, Diana
TITLE OF INVENTION: Yeast Promoter
CORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                 Sequence 2, Application US/08270076A; Patent No. 5667986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Swope, R. Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908/771-6159
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1483 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 908/771-6292
TELEFAX: 908/771-6159
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Best Local Similarity 55.9;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                       New Providence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 TCGTCCAA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Jersey
: USA
                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 07974
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Sequence 8, Application US/08512861A; Patent No. 6146886
08/337,608
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TELECHONICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-512-861A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCACGUCGGAAACGGU 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30.2%; Score 42.6; DB 3; Length 171; 67.6%; Pred. No. 2.4e-06; tive 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Lyon
              CMPUTER REALABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.5" Diskette, 1.44 Mb
MEDIUM TYPE: 5.0" DISKETE, 1.44 Mb
MEDIUM TYPE: 1.5" DISKETE, 1.44 Mb
MEDIUM TYPE: 1.44 Mb
MEDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215/154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 215/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: (67-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 67.6
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
GY: linear
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
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US-08-512-861A-10
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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28 AGCGUGCUGGGCCCCAUAACCCAGAGUCGAUGGAUGGAAACCCCGGA--UCGUACGGGG 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.2%; Score 41.2; DB 3; Length 146; 70.0%; Pred. No. 7.5e-06; Live 0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 CACAACACUGAUGAGGACCGAAAAGGUCCGAAACGGGCACG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCAGG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMFUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESD Version 1.5
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: August 8, 1995
PRIOR APPLICATION DATA: Two
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: NO. 6146886ember 10, 1994
ATTORNEY AGENT INFORMATION:
FILING DATE: NO. 6146886ember 10, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                           NAME: Warburg, Richard
REGISTRATION NUMBER: 32.7
REFERENCE/DOCKET NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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us-09-763-590-2.rni

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                                                                                     1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                           11 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGGAACGGTCCCCGG 70
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                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA TITLE OF INTENTION. RIBOZYME GENE THERAPY FOR HIV INFECTION AND ALDS CORRESPONDENCE: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
49.5%; Score 69.8; DB 3; Length 132; 72.6%; Pred. No. 2.9e-16; Live 18; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.5%; Score 69.8; DB 5; Length 133; 72.6%; Pred. No. 2.9e-16; tive 18; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= ""W = INTERNAL NUCLEOTIDE OTHER INFORMATION: SEQUENCE""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEN PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05700
FILING DATE: 17 MAY 1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: ROBBINS, BERLINER & CARSON STREET: 201 NORTH FIGUEROA STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5555-209
                                                                                                                                                                                                                                                                                                                     Sequence 17, Application PC/TUS9405700 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 6, Application US/08512861A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BERLINE, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-977-1001
TELEPHONE: 213-977-1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 72.69
Matches 53; Conservative
Query Match
Best Local Similarity 72.69
Matches 53; Conservative
                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 97
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: CALIFORNIA
RY: USA
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28 AUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAACCGGGCACUACAAACCAACA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGCCACGUCGGAAACGGU 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 30.2%; Score 42.6; DB 3; Length 171; Best Local Similarity 67.6%; Pred. No. 2.4e-06; Matches 75; Conservative 0; Mismatches 34; Indels ;
                                                              TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 80ite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION:
APPLICANT: UNDERSON: Thompson
TITLE OF INVENTION: MPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: AUGUST 8, 1995
PRIOR PELICATION DATA:
APPLICATION NUMBER: 08/293,520
FILING DATE: AUGUST 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886ember 10, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,327
                   GENERAL INFORMATION:
APPLICANT: James D. Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                Los Angeles
Californía
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STATE: California
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US-08-512-861A-6
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; Patent No. 6146886
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                                                                                                                                                                                                                                                                                                        90071
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                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
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                                                                                                                                                                                                                                             11 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACACGCAACGGTCCCCGG 70
                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. Johnson

GENERAL INFORMATION:
APPLICANT: Wong Staal, Flossie
APPLICANT: Yamada, Osamu
APPLICANT: Yamada, Osamu
APPLICANT: Leavitt, Mark
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
TITLE OF STOURDNIES: 18
                                                                                                                             49.5%; Score 69.8; DB 1; Length 132; 72.6%; Pred. No. 2.9e-16; tive 18; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCETWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,483 FILING DATE: 05-JUN-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,742
FILING DATE: 17-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEDEY: Keneth A.
REGISTERATION NUMBER: 31,677
REGISTERATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: -
LOCATION: (96~97)
OTHER INFORMATION: /note= "insertion location of
    /note= "insertion location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One Market Plaza, Steuart Street Tower
                      foreign gene in pol III transcription cassette in vector pMJT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence 17, Application US/08465483 Patent No. 5811275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPENDE: (415) 543-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                      61 UUCGAAACCGGGC 73
                                                                                                                                                                                                                                                                                                                                53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San Francisco
California
); OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
)
US-08-245-742A-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X: USA
94105-1492
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-465-483-17
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                                                                                                                                                                           Matches
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1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                             11 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAACGGTCCCCGG 70
                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Woog-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Ojwang, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
NUMBER OF SEQUENCES: 18
                                                                                                      49.5%; Score 69.8; DB 1; Length 132; 72.6%; Pred. No. 2.9e-16; Live 18; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "insertion location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/876,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Townsend and Townsend and Crew
One Market Plaza, Steuart Street Tower
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transcription cassette in
vector pMJT"
  foreign gene in pol III transcription cassette in vector pMJT"
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; Patent No. 6132962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                53; Conservative
                                                                                                                                                                                                                                                                        61 UUCGAAACCGGGC 73
                                                                                                                                                                                                                                                                                                               71 TTCGAAACCGGGC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 132 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco
California
) OTHER INFORMATION:
) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-465-483-17
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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STREET: Or
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STATE:
                                                                                                             Query Match
                                                                                                                              Best Local
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Sequence 1, Appli
Sequence 947, Appli
Sequence 7, Appli
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Sequence 111, Appli
Sequence 607, Appli
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Sequence 3, Appli
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Sequence 17, Appl
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Sequence 4, Appli
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                                                                                                                                             September 13, 2003, 07:56:11; Search time 47.5109 Seconds (without alignments) 1309.911 Million cell updates/sec
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    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
    /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
    /cgn2_6/ptodata/2/ina/BE_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-465-463-17

US-08-476-966-17

US-08-512-861A-6

US-08-512-861A-10

US-08-512-861A-14

US-08-512-861A-14

US-08-512-861A-14

US-08-512-861A-14

US-08-512-861A-14

US-08-512-861A-14

US-08-512-861A-14

US-09-198-423A-1

US-09-198-423A-1

US-09-198-423A-1

US-08-998-416-947

US-08-998-416-111B-1

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US-09-336-115C-1
US-09-453-702B-79
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   OM nucleic - nucleic search, using sw model
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4887 1 0
4792 4 0
1664976 4
648 3 0
729 3 0
1664976 4
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22.0 6488
20.0 1664976
20.0 1664976
20.1 16883
20.3 124883
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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 16, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 2, Appli
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Sequence 11, Appl
Sequence 134, Appl
Sequence 98, Appl
Sequence 98, Appl
Sequence 98, Appl
Sequence 93, Appl
Sequence 93, Appl
                                                                                                             Sequence 20,
Sequence 96,
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wong-Staal, Flossie
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Jamada, Osamu
APPLICANT: Ojamay, Joshua O.
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT GSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,742A
FILING DATE: 17-MAY-1994
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: WEDER: NTORMATION:
NAME: WEDER: NTORMATION:
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 33,077-567-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Townsend and Townsend and Crew
One Market Plaza, Steuart Street Tower
                                                                                                       US-08-150-204E-96
US-08-150-204E-96
US-09-009-217-11
US-08-09-217-11
US-08-311-731A-134
US-08-59-252-98
PCT-US-06-06582-98
PCT-US-06-06583-98
US-09-171-461-1
US-08-173-508-3
US-08-265-310-3
US-08-951-742-3
US-08-465-640-1
US-08-408-78-16
US-09-103-840A-2
US-09-103-840A-1
                                                                                                                                                                                                                    US-08-861-774E-93
                                                                                                                                                                                                                                 US-09-103-840A-2
                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08245742A; Patent No. 5670361; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
 LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend &
STREET: One Market Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (16,96)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94105-1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                 RESULT 1.
US-08-245-742A-17
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//Lione_Lib="Adult worms"
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1 (bases 1 to 543)

1 (W. Yan, Q., Shen, D., Liu, F., Xu, X., Zhu, Z., Zhang, X., Wang, J., Sun, J., Xu, X., Wang, Z., Zeng, L., Rong, Y., Wu, X., Qu, J., Xu, Z., Huang, J., Ma, Y., Wang, S., Wang, Z., Xue, C., Feng, Z., Chen, Z. and Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            have found that a small percentage, 2% to 3%, of the clones contain inserts that appear to be highly homologous to sequences from salmonoid fishes, as determined by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU712126 543 bp mRNA linear EST 12-FEB-2003 SJARAWA07 Adult Sjc 7/94 Schistosoma japonicum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homology comparisons using BLAST and by Southern hybridization analysis to genomic DNA from salmon (Sigma Chemical Co., St. Louis, MO) under stringent washing conditions. The remainder of the clones appear to contain
                                          this directional library by Clontech, it was returned to the QIMR. During analysis of the library at the QIMR, we
1 ACCGUUGGUUUCCGUAGUGUAGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Januese National Human Genome Center at Shanghai 201203, P. R. China Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed sequence tags from adults of Schistosoma japonicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schistosoma japonicum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Chinese (Anhui) strain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S. japonicum sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:6182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: hanzg@chgc.sh.cn,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU712126
BU712126.1 GI:28319513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schistosoma japonicum
Schistosoma japonicum
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479 TTCGAGCCCGGGC 467
                                                                                                                                                                         61 UUCGAAACCGGGC 73
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ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
BU712126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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1 others

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183 a

BASE COUNT

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64
                                                                                            5 UUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGGUUCG
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Query Match 46.4%; Score 62.6; DB 13; Length 543; Best Local Similarity 69.6%; Pred. No. 3.6e-10; Matches 48; Conservative 17; Mismatches 4; Indels 0;
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Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                         8 GUUUCCGUAGUGGAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGGUUCGAAA 67
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Ciona intestinalis genomic fragment, clone 3E10, genomic survey
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Vector: pBluesoribt KS.
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                                                                                                                                              /note="Genoscope sequence ID : C0AG219CH01SP1~end
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genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers
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                                                             /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
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Science 283 (5405), 1164-1167 (1999)
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/db_xref="taxon:99883'
/clone="219901"
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Ciona intestinalis
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AJ227180.1 GI:2951004
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/mol_type="genomic DNA" /db_xref="taxon:7719"

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GSS 03-DEC-2000
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Phlebobranchia; Cionidae; Ciona.
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Clark, V.H., Leitgeb, S., Charlton, J., Tweedie, S., Simmen, M.W. and
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Ciona intestinalis genomic fragment, clone 11G6, genomic survey
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Vector: pBluescript KS.
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tive 17; Mismatches 6; Indels 0
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/db_xref="taxon:7719"
/clone="11G6"
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Matches 50; Conservative
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage:
BP 1910 06 EVRI cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr
- Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequenching project of the Tetraodon nigroviridis penome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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/note="Genoscope sequence ID : Claa007zD04Cl-end : T7"
/ 202 c 217 g 347 t 19 others
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Protecanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
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Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
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/db_xref="taxon:99883"
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Best Local Similarity 74.2%
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                                                                                                                                                                                      Genoscope
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CNS0124U
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 21901 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                   /clone_lib="AGENAE Rainbow trout multi-tissues subtracted library (tcay)" /note="Vector: p1773D-pac; Clone distribution : AGENAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Pizames, C., Fischer, C., Boureau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE"
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                                                                       /clone="tcay0002b.i.04"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="bH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.6%; Score 64.2; DB 13; Length 595; 71.0%; Pred. No. 1.1e-10; Live 17; Mismatches 3; Indels 0;
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Genome Res. 10 (7), 939-949 (2000)
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/organism="Oncorhynchus mykiss"
                      /mol_type="mRNA"
/db_xref="taxon:8022"
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Tetraodon nigroviridis
Tetraodon nigroviridis
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//clone_lib="RRCI-23"
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
//note_2: EcoRi; Female C57BL/61 mouse kidney and/or
//brain genomic DNA was isolated and partially digested
//with a combination of EcoRi and EcoRi Methylase. Size
//selected DNA was cloned into the pBACe3.6 vector at the
//broin sites. The ligation products were transformed into
//broin sites. The ligation products were transformed into
// DHIOD electrocompetent cells (BRL Life Technologies). "
// St 9 66 t
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
                                                                                                                                                                                        Email: szhadetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/cofderingframe.htm)
or from Resea ch Genetics (info@resean.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 16 row: D column: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                            Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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  Mouse BAC End Sequences from Library RPCI-23
Unpublished
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Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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Other_GSSS: RPCI-23-144M11.TV
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ288311.1 GI:9530097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                          Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 CCGGGC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1
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JOURNAL
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/lab_nosu-naive.
/clone_lib="RepC1-23"
/clone_lib="RepC1-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRi; Site_2: BcoRi; Female c57BL/65 mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRi and EcoRi Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRi sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                         library availability, please contact Pieter de Jong Pieterdedoron, med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 144 row: M column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                          Email: szhao¢tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.7%; Score 64.4; DB 28; Length 574; 74.2%; Pred. No. 9.2e-11; tive 16; Mismatches 1; Indels 0;
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       letradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 574
1. 574
Mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="RPCI-23-144M11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS; genome survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL306891.1 GI:8208133
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_70013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Blood"
/clone_lib="CHORI-240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Initiative)
Plate: 70 row: 0 column: 13
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                 Other_GSSs: CH240_70013.TV
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Az115558
Az115558.1 GI:7776690
GSS.
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Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
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                                                                                                                         Genome Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.hax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymerase are to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4722114[jb]ART29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the linsert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CH240_70013.IJ CHORI-240 bp DNA linear GSS 12-JUN-2003 genomic survey sequence.
                                        Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_hosmar. coli strain XL10-Gold, T1-resistant, F-"
/lab_mouse 10kb plasmid UGGCM library"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus G57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAA 67 | 1::|||:||:||:||:||:||||| | 362 GTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTTCGAAA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0273 row: K column: 10
                                                                                                                                                                                                                                                  Plate: 0273 row: K column: 10
Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="c57BL/63"
                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 695.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="UUGC2M0273K10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Female"
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                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
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plasmid inserts
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Bos taurus
                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                   source
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BZ920607/c
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pp δλ

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l (bases 1 to 201)
LarKin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P.,
Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L.,
Womack,J.E., de Jong,P.J. and Lewin,H.A.
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 598
Tel: 217 233 598
Tel: 217 233 598
Tel: 217 233 598
Tel: 217 234 5617
Email: h-lewinGuluc.edu
Clones are derived from the bovine BAC library CHORI-240
Clones are derived from the bovine 240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Chttp://www.chori.org/bacpac/ordering.information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by by University of Illinois at Urbana Champaign
USDA-CSREES and Ac99-35205-8534 from USDA/NRI (Livestock Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 232)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.7%; Score 64.4; DB 29; Length 201; 74.2%; Pred. No. 7.2e-11; Live 16; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                             Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
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695 bp DNA linear GSS 27-APR-2001 2M0273KIOF Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0273KIO F, genomic survey sequence. A2989726 A2989726 GI:13860953 GSS.
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 30). Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 695)
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Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                            Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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  sapiens genomic clone Plate=2182 Col=10 Row=P, genomic survey
                                                                                                                                                                                                                                                                                                                                          scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.4%; Score 65.4; DB 28; Length 390; 74.6%; Pred. No. 3.9e-11; tive 16; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High Throughput Sequencing Center
University of Mashington
Joll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Plate=2182 Col=10 Row=P"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Mahairas GG, Wallace JC, Hood L
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/db_xref="taxon:9606"
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Location/Qualifiers
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Plate: 2182 row: P colum
Class: BAC ends
                                                AQ030852.
AQ030852.1 GI:3275778
                                                                                                                           Homo sapiens (human)
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Best Local Similarity
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                                                                                                                                                        Homo sapiens
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KEYWORDS
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A2989726
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Shacks, Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
Shacks, Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn
A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., de
Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
Unpublished
Other_GSSS: CH230-17997.TJ
Contact: Shaying Lano
Department of Entaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: schaoetigr.org
Chones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                        BH305888 720 bp DNA linear GSS 30-NOV-2001 CH230-179P7.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH330-179P7, genomic survey sequence.
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HS_2182_BZ_H05_MF CIT Approved Human Genomic Sperm Library D Homo
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/clone_lib="CHORI-230 Segment 1"
/note="Vector: pTaRBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CGUUGGUUUCCGUAGUGGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUU 62
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
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/clone="CH230-179P7"
                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
Rattus norvegicus
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/cell_type="Brain"
462 GAAACCGGGCGGAAACAA 445
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179 c 15
                                                                                                                                                                                                                                                 BH305888.1 GI:17218296
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AQ030852
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/lab_host="DH10B"
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                                                                                     /sex="Female"
                                                                                                                                                                                                                                                                                                                      1 Similarity 68.8% 55; Conservative
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Best Local Similarity
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BX132357/c
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                                                                            AZ062238 582 bp DNA linear GSS 30-MAR-2000 RPCI-23-404J7, TV RPCI-23 Mus musculus genomic clone RPCI-23-404J7, genomic survey sequence.
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
and Fraser,C.M.
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1 (bases 1 to 582)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CCGUUGGUUUCCGUAGUGUAGGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGU 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (Pieter@dejong.med.buffalo.edu), Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 UCGAAACCGGGCACUACAAACACACGGAGGAGGACCGAAAGGUCCGAAA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%; Score 71; DB 10; Length 464; 62.5%; Pred. No. 5.6e-13; Live 16; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    5,6e-13;
ches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSS: RPCI-23-404J7.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse BAC End Sequences from Library RPCI-23
                                /organism="Homo sapiens"
                                                                /db_xref="taxon:9606"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                 _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ062238
AZ062238.1 GI:7353487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.58
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: T7
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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JOURNAL
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AZ062238
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FEATURES
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/doce_lib="RECI-23"
/foloe_lib="RECI-23"
/foloe_lib="RECI-23"
/foloe="Organ: Kidney/Brain; Vector: pBACe3.6; Site_l:
Excorl; Femala C57BLf-65 mouse kidney and/or
brain genomic DAR was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DAR was cloned into the pBACe3.6 vector at the
selected DAR was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

a 125 c 163 g 140 t
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1 (bases: Lo 767)
Humphray, S. J., Huckle, E. and Durham, J. L.
Direct Submission
Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS 28-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campus, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 90F23, 90F23
part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Danio rerio genomic clone DKEY-90F23, genomic survey sequence.
BX132357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.8%; Score 67.2; DB 28; Length 582; 68.8%; Pred. No. 1.1e-11;
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/note="vector pindigoBAC-536"
1 144 c 121 g 258 t
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/clone="RPCI-23-404J7"
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/db_xref="taxon:7955"
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Page 1

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September 13, 2003, 09:43:56 ; search time 1900.27 Seconds (without alignments) 1726.650 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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BF244354 601862918 AZ062238 RPCI-23-4 BX132357 Danio rer BH305888 CH230-179

BF244354 AZ062238 BX132357 BH305888

10 28 29 28

464 582 767 720

52.6 49.8 49.5 49.0

71 67.2 66.8 66.2

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Description

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Query Match Length DB

Score

No.

Result

5 65.4 48.4 390 28 AQ030852 6 64.8 48.0 695 28 AZ989726 7 64.4 47.7 201 29 BZ920607	3 64.4 47.7 23.2 8 AZ288311 9 64.4 47.7 1101 29 CNS04TSI AZ288311 64.2 47.6 595 13 BX297643 BX297643 2 63.6 47.1 206 29 CNS0124U AL3297643 63.6 47.1 206 29 CNS0124U AL3273847 63.4 47.0 617 29 C13E10 AJ2227180	62.6 46.4 543 13 BU712126 BU71224 BU711524 BU711528 BU711524 BU711528 BU711	2 61.6 45.6 1101 29 CNS05MY AL346799 TECTRAGORD C 24 61.2 45.3 467 9 AA489977 AA4897	35 58.6 43.4 987 29 CNSO56OS AL315829 36 58.4 43.4 100.2 29 CNSO56ED AL7423333 38 58.4 43.3 610 29 DR.6F6S AL745338 38 58.2 43.1 946 29 CNSO281P AL105539 40 58 43.0 38 13 BW366352 BW166952 41 58 43.0 363 13 BW366387 BW266387 43 57.2 42.4 935 29 CNO9551 BH0663631 44 56.2 41.6 791 29 CC127410 CC127410 45 55.8 41.3 819 29 BX232148 BX2332148 ALIGNMENTS	RESULT 1 BF244354 LOCUS DEFINITION 601862918F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4080340 5', RNAM sequence. ACCESSION BF244354.1 GI:11158272 REYMORDS SOURCE ORGANISM Hemo sapiens (human) ORGANISM Homo sapiens (human) AUTHORS I (bases 1 to 464) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITILE ORDALISM FX SOBERT STRAUSDERG, Ph.D. Email: cgapbs:r@mail.nih.gov TISSUE PROCUEMENT: AROBET STRAUSDERG, Ph.D. Email: cgapbs:r@mail.nih.gov TISSUE PROCUEMENT: AROBET STRAUSDERG, Ph.D. Email: cgapbs:r@mail.nih.gov TISSUE PROCUEMENT: Arged by: Incyte Genomics, Inc. CONMENT Experiment: Arged by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Search completed: September 13, 2003, 09:43:36 Job time : 166.25 secs

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RESULT 15
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LENGTH: 999
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                                                                                                                                                                                                                                                                                                              APPLICANT: Huang, Tim
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILE REFERENCE: UMO1523
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CURRENT FILING DATE: 2002-02-1
FRIOM PEPLICATION NUMBER: 06/120,592
FRIOM PELING DATE: 1999-02-18
FRIOM APPLICATION NUMBER: 06/118,760
FRIOM PILING DATE: 1999-02-05
NUMBER OF EQ ID NOS: 54
SOFTWARE: Patentin Version 3.0
LENGTH: 118067
TYPE: DNA
TYPE: DNA
CORGANISM: HOMO Sapiens;
                                                                                                                                                                                                          ; Sequence 32, Application US/10081327
; Publication No. US20030129602A1
; GENERAL INFORMATION:
44530 CTGG 44533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                  RESULT 12
US-10-081-327-32
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29.8%; Score 40.2; DB 13; Length 322; 51.9%; Pred. No. 0.00014;

Query Match Best Local Similarity

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Sequence 100, Application US/09842552
Patent No. US20020055628A1
GENERAL INFORMATION:
APPLICANT: The PROGRATION:
TITLE OF INVENTION: RELATED BACTERIA
FILLE REFERENCE: S-99,687
CURRENT APPLICATION NUMBER: US/09/842,552
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/199,911
PRIOR PILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 106
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Malven, Marianne
APPLICANT: Malven, Marianne
APPLICANT: Masucci, James D.
TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL OF GENE EXPRE
FILE REFERENCE: 38-21 (51703) A
CURRENT APPLICATION NUMBER: US/10/325,107
UNMBER OF SEQ ID MOS: 68
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                                                               7 GGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAA 66
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  Gaps
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23; Indels
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40; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                     ; Sequence 59, Application US/10325107; Publication No. US/2030105947A1
; PENERAL INFORMATION:
; APPLICANT: Dubois, Patrice
                                                                                                                                                                         151 ACTCAACGGAAACAACA 167
                                                                                                                              67 ACCGGGCACUACAACA 83
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Best Local Similarity 53....
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US-10-325-107-59/c
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PRIOR FILING DATE: 2000-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITTLE OF INVENTION: Polymorphisms in the Human Genome
FITTLE SEPERANDE: 10827.129
CURRENT APPLICATION NUMBER: US/10/27,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-4
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,38
PRIOR APPLICATION NUMBER: US 60/185,38
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRACESO FOR Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TILE REFRENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 3000-07-12
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                                            Query Match 45.3%; Score 61.2; DB 13; Length 818; Best Local Similarity 69.7%; Pred. No. 5e-12; Matches 46; Conservative 17; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 135532, Application US/10027632; GENERAL INFORMATION:
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Best Local Similarity 61.54
Matches 40; Conservative
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US-10-027-632-135520
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; ORGANISM: Human
US-10-027-632-135532
US-10-027-632-150960
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LENGTH: 603
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPRESENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
FRIOR FILING DATE: 2000-04-20
FRIOR PRIOR FILING DATE: 2000-04-20
FRIOR PRIOR PREDICATION NUMBER: US 60/198,676
FRIOR PRIOR PREDICATION NUMBER: US 60/193,483
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 2000-03-29
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 48.7%; Score 65.8; DB 13; Length 704; Best Local Similarity 71.8%; Pred. No. 1.1e-13; Matches 51; Conservative 17; Mismatches 3; Indels 0;
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13960
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Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human
US-10-027-632-13960
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LENGTH: 704
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                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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US-10-027-632-150959

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Sequence 10000, Application Us/1007632

MPRICAME: Name 1, David C 
MPRICAME: Name 2, David C 
MPRICAME MPRICAME NAME 3, DAVID C 
MPRICAME MPRICAME NAME 3, DAVID C 
MPRICAME NAME 3, DAVID C 
MPRICAME MPRICAME NAME 3, DAV
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3 CGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUU 62
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                  Sequence 13959, Application US/10027632 GENERAL INFORMATION:
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                                                                                                                                       241 CGAAACCGGGC 231
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US-10-027-632-13960/c
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US-10-027-632-13959
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             Sequence 17, Application US/09974974
Publication No. US20030013095A1
Publication No. US20030013095A1
Publication No. US20030013095A1
APPLICANT: Razunari TAIRA
APPLICANT: Macashi WARASHINA
APPLICANT: Tomoko WARASHINA
TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a TITLE OF INVENTION: target RNA by recognizing another molecule
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Sequence 13958, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide; TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 61.3%; Score 82.8; DB 11; Length 138; Best Local Similarity 97.7%; Pred. No. 5.9e-20; Matches 84; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FULING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1000-02-24
PRIOR FILING DATE: 1999-11-33
PRIOR APPLICATION NUMBER: US 60/165,363
PRIOR APPLICATION NUMBER: US 60/166,363
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER: OF SEQ ID NOS: 325720
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LENGTH: 704
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/974,974
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: JP 2000-313320
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 51; Conserva
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; ORGANISM: Human
US-10-027-632-13958
                                                                                                                                                                                                                                 FILE REFERENCE:
US-09-974-974-17
                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 17
LENGIH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-974-974-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: RNA
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301 YGCAGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACGCGAAAGGTCCCCGGTT 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PRILICE DATE: 2002-04-30
FRIOR PELICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/60/218,006
PRIOR PELING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1099-11-28
PRIOR FILING DATE: 1099-11-28
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
PRIOR PELING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR PRIOR PAGESTED FOR WINDOWN VERSION 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERENCE: 108827.12
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/218,66
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,483
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(without alignments)
2241.006 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1632420 segs, 1213878141 residues
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Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                        US-09-763-590-1
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                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*
/cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

SUMMARIES

Description	Ϊ.	Sequence 5, Appli	Sequence 17, Appl	Sequence 13958, A	Sequence 13959, A	Sequence 13960, A	Sequence 13961, A	Sequence 150959,	Sequence 150960,	Sequence 135532,	Sequence 135520,	Sequence 148440,	Sequence 32, Appl	Sequence 272410,	Sequence 59, Appl	Sequence 100, App	Sequence 102, App
qi		US-09-974-974-5	US-09-974-974-17	US-10-027-632-13958	US-10-027-632-13959	US-10-027-632-13960	US-10-027-632-13961	US-10-027-632-150959	US-10-027-632-150960	US-10-027-632-135532	US-10-027-632-135520	US-10-027-632-148440	US-10-081-327-32	US-10-027-632-272410	US-10-325-107-59	US-09-842-552-100	US-09-842-552-102
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Length DB	1 0	88	138	704	704	704	704	818	818	603	817	871	118067	322	2126	666	2336
% Query Match		61.3	61.3	48.7	48.7	48.7	48.7	45.3	45.3	37.5	37.0	35.9	30.8	29.8	28.6	27.9	27.9
Score	1 0	8.7.8	82.8	65.8	65.8	65.8	65.8	61.2	61.2	50.6	20	48.4	41.6	40.2	38.6	37.6	37.6
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RESULT

Sequence 2, Appli Sequence 846, App Sequence 10165, A Sequence 3707, Ap Sequence 87, Appl	Sequence 3777, Ap Sequence 3809, Ap Sequence 3114, Ap Sequence 3628, Ap	3736, 3736, 3687, 3571, 608,	Sequence 1, Appli Sequence 23, Appl Sequence 23, Appl Sequence 1096, Ap Sequence 1, Appli Sequence 5, Appli	Sequence 6550, Ap Sequence 1, Appli Sequence 3, Appli Sequence 199164, Sequence 1, Appli Sequence 1, Appli Sequence 526, Ap Sequence 251, Appli Sequence 251, Appli Sequence 251155,
111 99 88		8 US-08-78 8 US-08-78 8 US-08-78 8 US-08-78	10 US-09-738-626- 12 US-10-056-405-2 14 US-10-094-240-2 12 US-10-311-455-1 14 US-10-156-761- 10 US-09-863-040-5	14 US-10-156-761-6550 10 US-09-954-973-3 13 US-10-027-632-199163 13 US-10-027-632-199164 9 US-09-970-711-1 14 US-10-156-761-556 13 US-10-027-632-251155 13 US-10-027-632-251156
5048 740 440 400 9425	400 400 6591 214	400 440 619 687	3309400 11103 11103 7690 9025608 4792	816 9025608 585 581 611 43804 786 1058
27.7 26.8 26.7 26.5	2225 225 25 25 25 25 25 25 25 25 25 25 2		24. 23.9 23.9 23.9 22.1 22.5 3	21.3 21.3 21.0 21.0 20.0 20.4 20.4 20.4
37.4 36.2 36.3 35.8	34 .8 34 .8 34 .8	3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	33 32.2 31.2 31.2 30.4	28.8 22.88.8 22.88.4 22.87.7 20.77.7 6
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ALIGNMENTS

Search completed: September 13, 2003, 08:05:55 Job time: 67.4891 secs

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US-07-789-915A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.4%; Score 31.6; DB 3; Length 702; 47.1%; Pred. No. 0.062; tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Baker, Rohan T.
APPLICANT: Baker, John W.
APPLICANT: Tobias, John W.
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/789,915A
FILING DATE: 19911108
CLASSIETCATION: 43.5
ATTORNEY AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: MIT-5091AA
TELECOMMUNICATION INPRESE: MIT-5091AA
                                                                                                                        PF/5-30306/A/CGC1976
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                            REFERENCE/DOCKET NUMBER: 35,241
REFERENCE/DOCKET NUMBER: PF/5-
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-8689
INFORMATION FOR AMERICAN FOR AME
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; Sequence 7, Application US/07789915A
; Patent No. 5212058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
:: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 4887 base pairs
                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 94
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 617-861-9540
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.18
Watches .33; Conservative
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CITY: Lexington
STATE: Massachusetts
                                      NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 1278..4013
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US-08-998-416-947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 GAAACCGGGC 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Baker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: line
MOLECULE TYPE: I
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
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                                                                                                                                                                                                                5 UNGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 UUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCG 64
                                                                                                                0; Gaps
Query Match 22.7%; Score 30.6; DB 1; Length 4887; Best Local Similarity 46.4%; Pred. No. 0.27; Matches 32; Conservative 13; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 22.7%; Score 30.6; DB 1; Length 4887; Best Local Similarity 46.4%; Pred. No. 0.27; Matches 32; Conservative 13; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Baker, Rohan T.
APPLICANT: Tobias, John W.
APPLICANT: Varshavsky, Alexander
TITLE OF INVENTION: Ubiquitin-Specific Proteases
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION WINBER: US/08/005,002C FILING DATE: 15-JAN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: MIT-5091AAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,915
FILING DATE: 08-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kevin M. Farrell, P.C. STREET: P.O. BOX 999
CITY: YOR Harbor
STATE: Maine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08005002C Patent No. 5494818
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 207-363-0558
TELEFAX: 207-363-0528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: 1.ENGTH: 4887 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
FOCATION: 1278..4013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4187 ATCCTGGGC 4179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4187 ATCCTGGGC 4179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 AAACCGGGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                65 AAACCGGGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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US-08-005-002C-7/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U ZIP: 03911
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                Query Match
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NAME/KEY: misc_feature
LOCATION: (55501). (57000)
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NAME/KEY: misc_feature
LOCATION: (58501). (60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (600001). (61500)
CTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (735001)..(750000)
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                                        NAME/KEY: misc_feature
LOCATION: (420001)..(435000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (705001)..(720000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (72001)..(735000)
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LOCATION: (450001)..(465000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (690001)..(705000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (615001)..(630000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (630001)..(645000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (645001)..(660000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c or g or
                                                                                                        NAME/KEY: misc_feature
LOCATION: (435001)..(450000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (750001)..(765000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (765001)..(780000)
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Query Match 24.1%; Score 32.6; DB 4; Length 1230025; Best Local Similarity 54.5%; Pred. No. 0.36; Matches 30; Conservative 11; Mismatches 14; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mond. Christine
APPLICANT: Mondland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                  NAME/KEY: misc_feature
LOCATION: (780011)..(795000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (810001)..(825000)
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NAME/KEY: misc_feature
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (825001)..(840000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (855001)..(870000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
OTHER INFORMATION: n=a or c or g or
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/W8-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 947, Application US/08998416; Patent No. 6239264; GENERAL INFORMATION:
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PRIOR APPLICATION DATA.
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 24-DEC-1997
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-998-416-947/c
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us-09-763-590-1.rni

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NAME/KEY: misc_feature
LOCATION: (165001)...(180000)
LOCATION: (165001)...(180000)
NAME/KEY: misc_feature
LOCATION: (180001)...(195000)
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NAME/KEY: misc_feature
LOCATION: (195001)...(210000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (210001)...(210000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (210001)...(225000)
OTHER INFORMATION: n=a or c or g or t
COTHER INFORMATION: n=a or c or g or t
COTHER INFORMATION: n=a or c or g or t
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LOCATION: (255001)..(270000)
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NAME/KEY: misc_feature
LOCATION: (270001)..(285000)
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LOCATION: (285001)..(300000)
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NAME/KEY: misc_feature
LOCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (330001)...(345000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (345001)...(360000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (120001)..(135000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KET: misc_feature
LOCATION: (135001)..(150000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (150001)..(165000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (225001)..(240000)
OTHER INFORMATION: n-a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (315001)..(330000)
OTHER INFORMATION: n~a or c or g or t
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LOCATION: (39001)..(40500)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
                                                                              NAME/KEY: misc_feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
LOCATION: (75001)..(90000)
                                                                                                                                                                                                                                           NAME, KEY: misc_feature
LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g or t
  NAME/KEY: misc_feature
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                                                       LOCATION: (75001)..(90000)
OTHER INFORMATION: n-a or c or g or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGAAACCGGGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.5%; Score 34.4; DB 1; Length 1483; Best Local Similarity 55.9%; Pred. No. 0.0081; Matches 38; Conservative 9; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
// LOCATION: 123..124
USCATION: /product= "SstII restriction site"
US-08-270-076A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KET: misc_feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KET: misc_feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
                                                                                                                                                          FILING DATE: 18-0CT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/597,687
FILING DATE: 16-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,286
FILING DATE: 04-AUG-1992
ATORNEY/AGENT INFORMATION:
NAME: SWOPE, R. Hain
RECISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92R834-3
TELEPHONE: 908/771-6159
TELEPHONE: 908/771-6159
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,076A
FILING DATE: U1-U1-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: GB 8923521.2
FILING DATE: 18-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09198452A Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1483 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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LENGTH: 1230025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-198-452A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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Matches 39; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 488:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...186
SEQUENCE DESCRIPTION: SEQ ID NO: 488:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Enterococcus faecium
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 2, Application US/08270076A; Patent No. 5667986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 186 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 CCCGTCGGAACCGCCA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 CCGGGCACUACAAACA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-107-532A-488
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US-09-107-532A-488/c
Sequence 488, Application US/09107532A
Sequence 488, Application US/09107532A
Sequence 488, Application US/09107532A
Sequence 488, Application US/09107532A
Sequence 688, Application US/0910753A
Sequence 688, Application US/091075A
Sequence 6888, Application U
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                                                                                                                                                                                                                                            TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCACG 121
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ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 05/08/512,861A
FILING DATE: August 8, 1995
PRIOR APPLICATION DATA: Two
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886ember 10, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTERO VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215/154
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                                                                                             Sequence 8, Application US/08512861A Patent No. 6146886 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 21:
ELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,327
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COUNTRY: USA
                                                                                                                                                                                                          APPLICANT: James D. Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warburg, Richard
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                             RESULT 9
US-08-512-861A-8
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8 GUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGGUUCGAAA 67
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51.3%; Pred. No. 0.004;
tive 11; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Sleep, Darrell
APPLICANT: Goodey, Andrew R
APPLICANT: Goodey, Andrew R
APPLICANT: Goodey, Diana
ITILE OF INVENTION: Yeast Promoter
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: The BOC Group, Inc.
STREET: 100 Mountain Avenue, Murray Hill
CITY: New Providence
STRIE: New Jersey
COUNTRY: USA
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORIET AGENT THORNALION:
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TELEFAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                               LENGIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
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TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
TUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 00,1094
PILING DATE: AUGUST 19, 1994
APPLICANION NUMBER: 08/337,608
FILING DATE: No. 6146886ember 10, 1994
ATTORNEY AGENT INFORMATION:
NAME: WAIDING, Richard
REGISTRATION NUMBER: 22,327
REFERENCE/DOCKET NUMBER: 215/154
TELECHMONICATION INFORMATION:
TELECHMONE: (213) 489-1600
TELEFAX: (213) 955-0440
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APPLICATION NUMBER: 08/337,608
FILING DATE: No. 6146886ember 10, 1994
ATTORNEY/AGENI INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage COMPUTER: ENCOMPATIBLE COMPATIBLE COMPATIBLE STORAGE SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A FILING DATE: August 8, 1995
PRIOR APPLICATION DATA: TWO
APPLICATION NUMBER: TWO
APPLICATION NU
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIOR APPLICATION DATA: TWO
APPLICATION NUMBER: 08/293,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 215/154
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08512861A Patent No. 6146886 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warburg, Richard REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: nucleic acid
; STRANDEDESS: single
; TOPOLOGY: linear
US-08-512-861A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
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                                                    0; Gaps
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                                                                                                                         82 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCACGUCGGAAACGGU 132
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Query Match 29.5%; Score 39.8; DB 3; Length 171; Best Local Similarity 86.3%; Pred. No. 4.6e-05; Matches 44; Conservative 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.4%; Score 38.4; DB 3; Length 146; 97.5%; Pred. No. 0.00014; tive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                   Sequence 4, Application US/08512861A
Patent No. 6146886
GENERAL INFORMATION: THOMBSON
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 CACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCACG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette
OPERATING SYSTEM: IBM P.C. DOS 5.0
SUSRENT APPLICATION DATE: August 8, 1995
PRIOR APPLICATION DATE: Two
APPLICATION NUMBER: 08/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/337,608
FILING DATE: NO. 6146886ember 10, 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,327
RER: 215/154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: (7-3510
INFORMATION FOR SEC ID NO: 4:
SEQUENCE CHARACTERISTICS:
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1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ACCGTIGGTTTCCGTAGTGTAGTGGTTATACACGTTCGCCTCACACGCGAACGGTCCCCGG 70
                                                                                      1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                               APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA TITLE OF INVENTION: RIBOZYME GENE THERAPY FOR HIV INFECTION AND ALDS NUMBER OF SEQUENCES: 18
                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
51.7%; Score 69.8; DB 3; Length 132; 72.6%; Pred. No. 9.4e-16; tive 18; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 51.7%; Score 69.8; DB 5; Length 133; I Similarity 72.6%; Pred. No. 9.4e-16; 53; Conservative 18; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= ""W = INTERNAL NUCLEOTIDE OTHER INFORMATION: SEQUENCE""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: TBM FO COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05700
FILING DATE: 17 MAY 1994
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBBINS, BERLINER & CARSON
STREET: 201 NORTH FIGUEROA STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US94/05700
17 MAY 1994
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                                                                                                                                                                                                                                                                           RESULT 4
PCT-US94-05700-17
; Sequence 17, Application PC/TUS9405700
; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEFUNE: 213-977-1001
TELEFAX: 213-977-1003
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE GRARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: BERINER, ROBERT
REGISTRATION NUMBER: 20,121
                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 UUCGAAACCGGGC 73
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Matches 53; Conservative
                                                                                                                                                                       61 UUCGAAACCGGGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: LOS ANGELES
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-512-861A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
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78 CAAACACAACAUGAUGAGGACCGAAAGGUCCGAAACGGGCACGUCGGAAA 128
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90.2%; Pred. No. 3.4e-06;
tive 0; Mismatches 5; Indels
                                      APPLICANT: James D. Thompson
TITLE OF INVENTION: IMPROVED RNA POLYMERASE III-BASED
TITLE OF INVENTION: EXPRESSION OF THERAPEUTIC RNAS
WUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMPROVED RNA POLYMERASE III-BASED EXPRESSION OF THERAPEUTIC RNAS
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IN Compatible
COMPUTER: IN Compatible
SPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/512,861A
FILING DATE: August 8, 1995
PRIOR APPLICATION NUMBER: US/293,520
FILING DATE: August 19, 1994
APPLICATION NUMBER: 08/397,608
FILING DATE: No. 6146886ember 10, 1994
ATORNEY/AGENT INFORMATION:
NAME: WALBLEY RICHARD NUMBER: 32,327
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 215/154 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 6, Application US/08512861A; Patent No. 6146886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: James D. Thompson
TITLE OF INVENTION: EXPRESSIO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 67 3510
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.24
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 90071
; Patent No. 6146886
; GENERAL INFORMATION:
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US-08-512-861A-14
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US-08-512-861A-6
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US-08-876-996-17
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                                                                                                                                                                                                                                                       11 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTCACACCGGAACGGTCCCCGG 70
                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17. Application US/08465483
Patent No. 581275
GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yu, Mang
APPLICANT: Cjwang, Joshua O.
APPLICANT: Cjwang, Joshua O.
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and Alds
                                                                                                                                    51.7%; Score 69.8; DB 1; Length 132; 72.6%; Pred. No. 9.4e-16; Live 18; Mismatches 2; Indels (
/note= "insertion location of
foreign gene in pol III
transcription cassette in
vector pMJT"
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OTHER INFORMATION: /note= "insertion location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,483 FILING DATE: 05-JUN-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2307E-567-11
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APPLICATION NUMBER: US 08/245,742
FILING DATE: 17-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Weber, Kenneth A.
REGIZHATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 2307E
TELECOMMUNICATION INPORMATION:
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 132 base pairs
                                                                                                                                                            Best Local Similarity 72.6%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                               61 UUCGAAACCGGGC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: ONE MAINCE
CITY: San Francisco
CMATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                        US-08-245-742A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-465-483-17
                                                                                                                                         Query Match
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0
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                                                                                                                                                                                                      1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Manda, Osamu
APPLICANT: Tamada, Osamu
APPLICANT: Ojwang, Joshua O.
APPLICANT: Ojwang, Joshua O.
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                              51.7%; Score 69.8; DB 1; Length 132; 72.6%; Pred. No. 9.4e-16; tive 18; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower
foreign gene in pol III
transcription cassette in
vector pMJT"
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transcription cassette in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 23C
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 543-9600
TELEFAX: (415) 543-9601
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA ZIP: 94105-1492 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                Query Match 51.7%
Best Local Similarity 72.6%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                             61 UUCGAAACCGGGC 73
                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
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                          OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                       US-08-465-483-17
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Sequence 7, Appli
Sequence 1, Appli
Sequence 111, App
Sequence 5, Appli
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Sequence 10, Appl
Sequence 4, Appli
Sequence 8, Appli
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Sequence 1, Appli
Sequence 20, Appl
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Sequence 17, Appl
Sequence 14, Appl
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                                                                                                                                                                               September 13, 2003, 07:56:11 ; Search time 45.4891 Seconds
(without alignments)
1309.911 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-875-996-17
US-08-812-861A-14
US-08-512-861A-14
US-08-512-861A-10
US-08-512-861A-4
US-08-512-861A-4
US-09-107-532A-488
US-09-107-532A-488
US-08-270-076A-2
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3 US-08-998-416-947
1 US-07-789-915A-7
1 US-08-005-002C-7
1 US-08-487-203A-7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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	28	28	20.7	4411529	m	US-09-103-840A-1	Sequence I, Appli
υ	29	27.4	20.3	4403765	m	US-09-103-840A-2	sednence 7, Api
υ	30	27.4	20.3	4411529	m	US-09-103-840A-1	Sequence 1, Appli
U	31	27.2	20.1	5109	4	US-08-930-055A-2	Sequence 2, Appl
	32	27	20.0	61663	4	US-09-453-702B-62	Sequence 62, Ap
	33	26.6	19.7		Н	US-08-599-252-98	Sequence 98, App
	34	26.6	19.7		S	PCT-US96-06352-98	Sequence 98, Ap
	35	26.6	19.7	724	ខេ	PCT-US96-06583-98	Sequence 98, App.
υ	36	26.2	19.4		4	US-09-328-352-1239	Sequence 1239,
O	37	26.2	19.4	724	ന	US-08-961-083-45	Sequence 45, App.
U	38	26.2	19.4	724		US-09-536-784-45	45,
	39	26.2	19.4	16	4	US-08-961-527-52	
O	40	56	19.3			US-09-453-702B-96	Sequence 96, Appl
	4.1	36	19.3	49795	4	US-09-453-702B-60	Sequence 60, App]
Ų	42	25.8	19.1		4	US-09-438-268-3	Sequence 3, Appli
	43	25.8	19.1	4	~	US-08-614-770A-1	Sequence 1, Appli
	44	25.6	19.0	36	-	US-08-271-880A-224	Sequence 224, App
	45	25.6	19.0	36	?	US-08-910-408-224	Sequence 224, App

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Wong-Staal, Flossie
APPLICANT: Yu, Mang
APPLICANT: Yamada, Osamu
APPLICANT: Tamada, Osamu
APPLICANT: Leavitt, Mark
APPLICANT: Leavitt, Mark
APPLICANT: Ho, Anthony
TITLE OF INVENTION: Ribozyme Gene Therapy for HIV Infection
TITLE OF INVENTION: and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                     One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2307E-567-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,742A
FILING DATE: 17-MAY-1994
CLASSIFTCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/062,465
FILING DATE: 17-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
             ; Sequence 17, Application US/08245742A; Patent No. 5670361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Weber, Kenneth A.
REGISTRATION NUMERS: 31,67
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 132 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          STREET: One Mainer
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-MAY-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (66~94)
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US-08-245-742A-17
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PC
C12N15/09, A61K31/7105, A61K31/711, A61K38/00, A61K48/00, A61P31/12, PC
                                                                                                                                A61P43/00,
PC C12N9/22,C12Q1/02,C12Q1/68,G01N33/53,G01N33/566,C12N15/00, PC
                                                                                                                                                                    Description of Artificial Sequence: the sequence encoding CC tRNAval-TAR GUU
                                                                                                                                                                                                                                                                                                                                            is of a
KpnI-recognition site
Other information: the sequence of nucleotide numbers 138-309
is of CTE
                                                                                                                                                                                                                                                                                                                                                                                                                            is of an EcoRV-recognition site Other information: the sequence of nucleotide numbers 316-320
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                                                                                                                                                                                                                                                                          Other information: the sequence of nucleotide numbers 92-131 is of TAR GUU
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Artificial Sequence
JP 2001190282-A/11
17-JU-2001
02-NOV-2000 JP 2000336082
KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ______Natificial Sequence'. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 320.
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
19 c 81 g 67 t
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terminator
Key
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PD 17-J
PF 02-N
PI KAZU
KAWASAKI
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Search completed: September 13, 2003, 10:39:38 Job time : 1378.46 secs

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1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
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                                                                                 61 TTCGAAACCGGGCACTACAAAACCAACTTATCTGGTC 99
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Location/Qualifiers
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BD015618.1 GI:22556755
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synthetic construct
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nes 69; Conserv
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Matches
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BD015618
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JOURNAL
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AX138450
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Other information: the sequence of nucleotide numbers 147-151
is of a
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                                  SM synthetic construct
artificial sequences.

E 1 (bases 1 to 151)
S Talra,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
Slidable functional chimeric molecule
D Patent: UP 2001190282-A 10 17-JUL-2001;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MANABU NARAJIMA TECHNOLOGY, KAZUNARI TAIRA
OS Artificial Sequence
PN JP 2001190282-A/10
PD 17-JUL-2001
PP 02-NOY-2000 JP 200335082
                1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence of nucleotide numbers 92-131
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                                                                                                                                                                                                     linear
                                                                                   61 UUCGAAACCGGGCACUACAAACACACACGCGGGGGGC 99
                                                                                                   61 TICGABACCGGGCACTACARABACCBACTITATCTGGTC 99
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                       DNA
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Matches 69; Conserv
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BD015617
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sequence of nucleotide numbers 92-131 is of TAR GUU Rz.-Other information: the sequence of nucleotide numbers 132-137 is of a Kpnl-recognition site.-Other information: the sequence of nucleotide numbers 138-309 is of CTE.-Other information: the sequence of nucleotide numbers 138-309 is of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [ (bases 1 to 320)
Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
Slidable functional chimeric molecule
Patent: JP 201190282-A 11 17-JUL-2001;
DIRECTOR GENERAL. OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA
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Functional ribozyme chimeric molecules capable of sliding
Patent: EP 1097993-A 11 09-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.7%; Score 84.6; DB 6; Length 320; 69.7%; Pred. No. 7.5e-15; Live 21; Mismatches 9; Indels (
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/note="the sequence encoding tRNAval-linked TAR GUU
Rz-Other information: the sequence of nucleotide numbers
1-91 is of tRNAval with 3'-modification.-Other
information: the sequence of nucleotide numbers 92-131 is
of TAR GUU Rz.-Other information: the sequence of
nucleotide numbers 132-137 is of a kpn1-recognition
site.-Other information: the sequence of nucleotide
numbers 138-140 is of a linker.-Other information: the
sequence of nucleotide numbers 141-146 is of an
ECORV-recognition site.-Other information: the sequence of
nucleotide numbers 147-151 is of a terminator."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 UUCGAAACCGGGCACUACAAACACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biotechnology; 1-17-71, Fuchinobe, Sagamihara-shi 229-8501, Japan (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGG 60
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Functional ribozyme chimeric molecules capable of sliding
Patent: EP 1097993-A 10 09-MAY-2001;
Secretary of Agency of Industrial Science and Technology (JP);
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                                                                                                                                                                                     /product="tRNAval/anti-mSry ribozyme complex
                                                                                                                                                                                                                                                                                                                                                                                                            63.0%; Score 85; DB 12; Length 153; 60.9%; Pred. No. 5.7e-15; Live 22; Mismatches 30; Indels
                                                                                                                                                                                                                                /function="anti murine Sry ribozyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                              /organism="synthetic construct"
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Sequence 10 from Patent EP1097993.
AX138449
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/hote="derived from tRNA"
88. .153
                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:32630"
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                               BD143601 137 bp RNA linear PAT 17-JAN-2003
Method of selecting high-function nucleic acid molecule in cell.
BD143601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of Veterinary Medicine, Lab. Developmental and Reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 UUCGAAACCGGGCACUACAAACACAAACACGAGAGGACCGAAAGGUCCGAAACGGGCCAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACCGITGGITTCCGIAGIGTGAGGGTTATCACGITCGCCTAACACGCGAAAGGTCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                OS Artificial Sequence
PN UP 2002125685-A/2
PD 08-MAX-2002
PF 30-CCT-2000 JP 200331347
PI RAZUMARI TAIRA, MASATURI SANO
PC C12N15/09,C1229/06,C1201/02,C1201/25,C1201/68,C12N15/00 CC
Description of Artificial Sequence: Sequence of tRNA-Luc GUA CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tachi, C., Nakamaura, K., Horii, T., Murata, C., Nishimura, S., Nishino, K., Nakayama, A. and Taira, K. Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
                                                                                                                                                                                                        artificial sequences.

1 (Dass 1 to 137)

Taira,K. and Samo,M.

Method of selecting high-function nucleic acid molecule in cell

Patent. JP 2002125685-A 2 08-MAT-2002.

DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL

SCIENCE AND HIROSHI YATSUHASHI, TECHNOLOGY, KAZUNARI TAIRA
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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Tachi, C.
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Best Local Similarity 58.55
Matches 79; Conservative
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JP 2002125685-A/2.
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Expression system for functional nucleic acid transcription. B33214
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                        PAT 27-AUG-2002
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                                                                                  ENCE (bases 1 to 142)

Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
Sidable functional chimeric molecule
NAL Patent: JP 2001190282-A 53 17-JUL-2001;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND MANBUN WKAJIMA TECHNOLOGY, KAZUNARI TAIRA
OS Artificial Sequence
PD 17-JUL-2001
PP 02-NOW 2001
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Synthetic construct
Synthetic construct
Taineal sequences.

Tabira,K., Okawa,A. and Ozeki,S.
Tabira,K., Okawa,A. and Ozeki,S.
Parpression system for functional nucleic acid transcription
Batent: JP 200006992-A 12 07-MaR-2000;
AGENCY OF IND SCIENCE & TECHNOL
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                        linear
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
/db_37 c 37 g 29 t
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                      BD015660 142 bp RNA Slidable functional chimeric molecule.
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JP 2001190282-A/53.
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JP 2000069972-A/12.
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National Institute of Advanced Industrial Science and Technology
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                                                          KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI
C12N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
Key
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                                                                                                                                                                                                                                                                            63.3%; Score 85.4; DB 6; Length 109; 86.2%; Pred. No. 4.3e-15;
                                                                                                                       /organism='Artificial Sequence'
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/organism="synthetic construct"
/nol_type="mRNA"
/db_xref="taxon:32630"
/note="Sequence of tRNA_Luc GUA Rz"
                                                                                                                                                           1. .109
/organism="synthetic construct"
/mol_type="qenomic DNA"
/db_xref="taxon:32630"
? 29 c 30 g 32 t
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                                                                                                                                                                                                                                                                                                                                                                                                                            49 CGAAACGGCACGTCGGAAACGGTTTT 23
               07-MAR-2000
31-AUG-1998 JP 1998244755
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JP 2000069972-A/12
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Best Local Similarity 86.23
Matches 75; Conservative
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Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
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Submitted (27-FBB-2002) Chikashi Tachi, Azabu University School of
Veterinary Medicine, Lab. Developmental and Reproductive
Biotechnology, 1-17-71, Fuchinobe, Sagamihara-shi 229-8501, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGG 60
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YUTAKA TAKEBE, JUN OKAWA
CIZNI5/09,A61K31/711,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
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                            synthetic construct
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 175)
Takebe, Y. and Okawa, J.
Ribozyme expression system
Patent: JP 2002262880^A 5 17-SEP-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
YUTAKA TAKEBE, JUN OKAWA.
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Best Local Similarity 64.1%; Pred, No. 2.7e-16;
Matches 93; Conservative 26; Mismatches 16; Indels 10
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/organism='Artificial Sequence'
Location/Qualifiers
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/mol_type="genomic DNA"
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JP 2002262880-A/5
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Functional ribozyme chimeric molecules capable of sliding
Patent: EP 1097993-A 53 09-MAY-2001;
Secretary of Agency of Industrial Science and Technology (JP);
Taira, Kazunari (JP)
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                                                                                                                                          /product="tRNAval/anti-mSry ribozyme complex
anti-mSrytRNA/Rz6"
/function="anti murine Sry ribozyme"
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/mol_type="mRNA"
/db_xref="taxon:32630"
/note="the notelotide sequence of CPP Rz5"
37 g 29 t
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(E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
                                                          /organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                               /note="derived from ribozyme"
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+ive 22; Mismatches
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Sequence 53 from Patent EP1097993.
AX138492
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Expression system for functional nucleic acid transcription.
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1 (bases 1 to 142)

Tabira,K., Okawa,A. and Ozeki,S.

Expression system for functional nucleic acid transcription Patent: JP 200069972-A 2 07-WAR-2000;

AGENCI OF IND SCIENCE & TECHNOL
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C12N15/09, A61K31/70, A61K35/76, A61K48/00, C12N15/00 CC
Key
                                                           KAZUNARI TABIRA,ATSUSHI OKAWA,SHIORI OZEKI
CI2N15/09,A61K31/70,A61K35/76,A61K48/00,C12N15/00 CC
Key
                                                                                                      /organism='Artificial Sequence'.
Location/Qualifiers
                                                                                                                                                                                                                          100.0%; Score 135; DB 6; Length 136; 80.0%; Pred. No. 5e-30;
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                                                                                                                                                                                                                          Score 150,
Pred. No. 5e-30;
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/mol_type="genomic RNA"
/db_xref="taxon 32530"
1 38 c 37 g 28 t
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/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
35 c 37 g 28 t
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31-AUG-1998 JP 1998244755
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JP 2000069972-A/2.
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PAT 18-MAR-2003
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17-SEP-2002
09-MAR-2001 JP 2001067253
YUTAKA TAKEBE,JUN OKAWA
C12N15/09,A61K31/711,A61K35/76,A61K48/00,A61P31/18,C12N5/10,
C12N19/00,
C12N15/00,C12N5/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takebe, T. and Okawa, J.
Ribozyme expression system
Patent: JP 200226380-A 6 17-SEP-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
YUTAKA TAKEBE, JUN OKAWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels 11; Gaps
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    175
    organism='Artificial Sequence'.

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by JP 200226890-A/6
PD JT-SEP-2002
PF 09-MAR-2001 JP 2001067253
PI YUTAKA TAREBE, UN OKAWA
PC C12N15/09, A61X31/711, A61X35/76, A61X48/00, A
PC C12N15/00, C2 Description of Artificial Sequence: the
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/mol_type="qenomic DNA"
/db_xref="taxon:32630"
a 40 c 41 g 46 t
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BD174679
                                                                                                                                             115 GGGCACGUCGGAAACGGUUUU 135
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                                                                                                                                                                                                                                                                                                                 Ribozyme expression system.
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synthetic construct
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DEFINITION
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic.search, using sw model

Run on: September 13, 2003, 09:38:16; Search time 1374.46 Seconds

(without alignments)

e: GenEmbl:*

1: 9D_ba:*

2: 9D_htg:*

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11: 9D_xs:*

11: 9D_vi:*

12: 9D_vi:*

14: 9D_vi:*

15: em_fun:*

16: em_fun:*

17: em_hum:*

18: em_li:*

19: em_or:*

21: em_or:*

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23: em_pl:*

24: em_pl:*

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26: em_li:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		Query				
No.	Score	Match	Length	DB	ID	Description
Н	135	100.0	136	9	3320	3203
7	11	88.1	142	ω		204
m	ä	67.6	175	9	8	8
4 1	٠	66.2	175		BD174.679	BD174679 Ribozyme
ı, u		64.9	153		AB080624	380624
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ov.	S.	63.3	137		AX429079	AX429079 Sequence
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11	8	63.0	153		AB080619	AB080619 Synthetic
12	₹.	62.7	151		AX138449	S
13	₹.	62.7	151		BD015617	BD015617 Slidable
14	4.	62.7	320		AX138450	AX138450 Sequence
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0 7 0	•		000	ρl	AA433840	AA433846 Sequence
77	, i	δ1.3	æ (١٥	BD143502	BD143502 Nucleic a
7.7	· ·	61.3	88	ا ک	BD182356	BD182356 Novel max
23	ς,	61.3	100	0	E47174	E47174 Method for
24	ď	61.3	117	Q	BD174675	BD174675 Ribozyme
25	ς,	61.3	138	ø	AX453858	AX453858 Sequence
56	ď	61.3	141	9	AX138491	AX138491 Sequence
27	ά,	61.3	141	9	BD015659	BD015659 Slidable
28	d	61.3	142	9	AX138488	AX138488 Sequence
53	82.8	61.3	142	9	AX138489	AX138489 Sequence
30	ď	61.3	142	9	AX138490	AX138490 Sequence
31	ď	61.3	142	9	BD015656	BD015656 Slidable
32	ς.	61.3	142	9	BD015657	BD015657 Slidable
33	2	61.3	142	9	BD015658	BD015658 Slidable
34	78	57.8	128	9	E33205	E33205 Expression
35	73.4	54.4	149	9	E33207	
36	7	54.1	95	φ	4	
37	73	54.1	9.5	v	BD015615	
38	73	54.1	100	9	E33206)6 E3
39	73	54.1	100	-	631283	331283
4	73	54.1	1396	6		Human HtV1
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ALIGNMENTS

136 bp RNA linear PAT 31-JAN-2002	Expression system for functional nucleic acid transcription. E33203	.8623997	A/1.	struct	truct	quences.	136)	Tabira, K., Okawa, A. and Ozeki, S.	Expression system for functional nucleic acid transcription	Patent: JP 2000069972-A 1 07-MAR-2000;	AGENCY OF IND SCIENCE & TECHNOL
E33203	Expression system E33203	E33203.1 GI:18623997	JP 2000069972-A/1.	synthetic construct	synthetic construct	artificial sequences.	1 (bases 1 to 136)	Tabira, K., Okawa,	Expression system	Patent: JP 200006	AGENCY OF IND SCI
RESULT 1 E33203 LOCUS	DEFINITION ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	JOURNAL	

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Search completed: September 13, 2003, 09:52:32
Job time : 198.152 secs
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73..78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a ribozyme expression cassette comprising a tetracyclin operator, at least one promotor and a DNA sequence encoding a ribozyme successively from the 5' end. The tetracyclin operator is present at 2 to 10 nucleotides to 5' end from the transcription initiating site of the promotor. The expression cassette is useful in a method for preparing a cell having no sensitivity to HIV, and for inhibiting the growth of HIV. To illustrate the invention, a tet 01-human tRNAVal promoter cassette was constructed, using the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ACCGTIGGTTICCGTAGIGTAGIGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 88
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/note= "Forms a double-stranded region with nucleotides
                                                                                                                                                                                                                                                                                             Ribozyme expression cassette, useful for preparing a cell insensitive to HIV and for inhibiting growth of HIV, comprises a tetracyclin operator, at least one promotor and a sequence encoding a ribozyme successively from the upstream side -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 61.3%; Score 82.8; DB 25; Length 117;
Best Local Similarity 75.6%; Pred. No. Se-19;
Matches 65; Conservative 19; Mismatches 2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 117 BP; 31 A; 28 C; 26 G; 32 T; 0 other;
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/bound_moiety= "tRNA-val_T-MzL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 UUCGAAACCGGGCACUACAAACACAA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 15; 27pp; Japanese.
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                       09-MAR-2001; 2001JP-0067253
                                                                            09-MAR-2001; 2001JP-0067253
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                                                                                                                                                              TAKEBE Y.
                                                                                                                                                                                         (OKAW/) OKAWA J.
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The invention relates to a nucleic acid enzyme with modifiable RNA cleavage activity. More specifically the invention relates to a nucleic acid enzyme, trans maxizyme, which has selective and effective eradicating activity towards harmful cells by acquiring cleavage activity of a specific target RNA by recognition of the other RNA molecule. The enzyme of the invention is useful for cleaving target RNA and is useful in treating diseases caused by the target RNA. This polynucleotide sequence represents the tRNA-val T-WzL sequence related to the maxizyme enzyme of the invention.
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                                                                                                 /*tag= g // LRNA-val_T-MzL" // hound_moiety= "tRNA-val_T-MzL" // hote= "Forms a double-stranded region with nucleotides 11-4 of itself" // 95..107
/bound_molety= "tRNA-val_T-MzL"
/note= "Forms a double-stranded region with nucleotides
19-14 of itself"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A nucleic acid enzyme which has selective and effective eradicating activity towards harmful cells by acquiring cleavage activity of a specific target RNA by recognition of the other RNA molecule \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 61.3%; Score 82.8; DB 24; Length 138; Local Similarity 97.7%; Pred. No. 5.2e-19; les 84; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 138 BP; 31 A; 38 C; 32 G; 37 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GLJUTSU SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                       Human; maxizyme; target mRNA; helicase activity; viral disease; human immunodeficiency virus; HIV; hepatitis C; hepatitis B; cancer; apoptosis-associated disease; Alzheimer's disease; Parkinson's disease; autoimmune disease; inflammatory disease; genetic disorder; mRNA cleavage; virucide; nootropic; antiparkinsonlan; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a novel maxizyme that can bind to a target mRNA molecule or a molecule having helicase activity. The maxizyme is useful for the prevention and treatment of viral diseases such as human immunodeficiency virus (HIV), hepatitis C or hepatitis B, apoptosis-associated diseases such as Alzheimer's and Parkinson's diseases, cancer, autoimmune diseases, inflammatory diseases and genetic disorders. The maxizyme binds to and cleaves target mRNA irrespective of the higher-order structure of the latter. The present sequence represents a human RNA sequence relating to the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maxizyme binding to a molecule with helicase activity for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 61.3%; Score 82.8; DB 25; Local Similarity 97.7%; Pred. No. 4.6e-19; Les 84; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Warashina T, Warashina M, Kawasaki H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WALD-) NAT INST ADVANCED IND SCI & TECHNOLOGY. TAISHO PHARM CO LTD. (CRNO-) GENOPUNCTION INC.
                                                                                                                                                                                                                                                                                            Human RNA sequence relating to novel maxizyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       viral infection cancer and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; immunosuppressive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 UUCGAAACCGGCCACUACAAAAACCA 86
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                                                                                     61 UUCGAAACCGGCACUACAAAACCA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 30-31; 36pp; Japanese.
                                                                   61 UUCGAAACCGGGCACUACAAACACAA
                                                                                                                                                                                         BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-2002; 2002WO-JP04322.
                                                                                                                                                                                        ABX12785 standard; RNA; 88
                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200292821-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                         15-MAY-2003
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                                                                                                                                                                                                                        ABX12785;
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                                                                                                                                                                       ABX12785
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The present sequence is that of the human tRNA promoter sequences. to the invention for expression of the modified ribozyme sequences. The invention relates to a method for screening of in vivo active floozyme, comprising modification of a candidate ribozyme sequence taken from 8 hammerhead type ribozymes expected to cleave mRNA derived from the p16 gane and for screening for inhibition of expression of a cancer inhibitory gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.3%; Score 82.8; DB 22; Length 100;
                                                                                                                                   Human; Ribozyme; hammerhead type ribozyme; p16; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antiviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promotor; ribozyme; anti-HIV; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 100 BP; 30 A; 25 C; 21 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                     (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.6%; Pred. No. 4.8e-19; ive 19; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                        A screening method for active ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 UUCGAAACCGGGCACUACAAACACAA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tet 01-tRNAVal sequence, SEQ ID 1.
                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 3; 9pp; Japanese.
                          AAH47825 standard; DNA; 100 BP.
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                                                                                                          Human tRNA promoter sequence.
                                                                                                                                                                                                                                                                         99JP-0314579.
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                                                                              20-SEP-2001 (first entry)
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Matches 65, Conservative
                                                                                                                                                                                                                                                                                                                              WPI; 2001-373027/39.
                                                                                                                                                                                          JP2001128682-A.
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                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                 05-NOV-1999;
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                                                                                                                                                                                                                     15-MAY-2001.
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                                                      AAH47825;
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RESULT 13
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              AAH47825
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Unidentified.
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                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribozyme expression vector of the invention. The cassette comprises the human placental tRNAval promoter (see AAF90356), with a 3' modification, a DNA sequence corresponding to HIV-1 constitutive transport element (CTE, see AAF90354), and a 3' constitutive transport element (CTE, see AAF90354), and a 3' constitutive transport element (CTE, see AAF90354), and a 3' constitutive transport element (CTE, see AAF90354), and a 3' constitutive transport element (CTE, see AAF90354) and a 3' constitutive transport element CTE, and mason Pfizer monkey virus. Chimeric molecules of the invention include ribozymes such as TAR GUU Rz linked to a CTE, and a claimed method to prevent or treat viral diseases, diseases as sosiciated with apportant or treat viral diseases, diseases as expression. They are also used in a claimed method of gene expression. They are also used in a claimed method of gene expression or a gene associated with apportaily a viral of the CTE facilitates cleavage of RNA previously considered refractory because of local structure.
disease, comprises region with binding affinity for molecule capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid enzyme having allosteric RNA-cleaving activity, used for treatment of chronic myeloid leukemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid enzyme; maxizyme; allosteric RNA-cleaving activity; RNA cleavage; chronic myeloid leukemia;
Philadelphia chromosome abnormality; ss.
                                                                                                   The present sequence is that of a DNA cassette forming part of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 62.7%; Score 84.6; DB 22; Length 320; l Similarity 69.7%; Pred. No. 1.6e-19; 69; Conservative 21; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 UUCGAAACCGGGCACUACAAACACAACACUGAUGAGGAC 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 320 BP; 93 A; 79 C; 81 G; 67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hitoshio A;
                                                          Example 1; Page 13; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 55; 93pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of tRNA-val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP01187.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-551415/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCGUGGGUUCCCGUAGGGGUAGGGGUAGCACGUCGCCUAACACACGCGAAAGGUCCCCGG 60
                            left and right arms of a nucleic acid enzyme (maxizyme). The maxizyme has allosteric RNA-cleaving activity on a specific target RNA. The maxizyme can be used for efficient cleavage of RNA molecules at specific points, especially for the prevention and treatment of chronic myeloid lenkemia and Philadelphia chromosome abnormality. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A nucleic acid enzyme which has selective and effective eradicating activity towards harmful cells by acquiring cleavage activity of a specific target RNA by recognition of the other RNA molecule .
The specification describes nucleotide sequences which make up the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                         61.3%; Score 82.8; DB 20; Length 88; 97.7%; Pred. No. 4.6e-19; Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 88;
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97.7%; Pred. No. 4.6e-19;
live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
                                                                                                                                                                                                                                                                                                            Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maxizyme related tRNA-val promoter sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 UUCGAAACCGGGCACUACAAAACCA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAL40450 standard; tRNA; 88 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trans maxizyme; tRNA-val; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-0CT-2000; 2000JP-0313320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-OCT-2000; 2000JP-0313320.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (9-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 97.7 Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-483792/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 84; Conserve
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(TAIR/) TAIRA K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF90358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            faira K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF90358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A COOK WAX A COOK A COO
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                                                                                                         0;
                                                                                                                                                                                                                                                            UUCGAAACCGGGCACUACAAAAACCAACUUVAUUCCGCGCUGAUGAGGCCGAAAGGCCGA 120
                                                                                                                                                                                                                                 61 UUCGAAACCGGGCACUACAAACACAACACUGAUGAGGACCGAAAGGUCCGAAACGGGCAC 120
                                                                                                                                                 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                       1. ACGGUUSGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel chimeric molecule useful for clarifying biological function of target nucleic acid and for treating viral diseases, and Alzheimer's disease, comprises region with binding affinity for molecule capable of
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of a DNA cassette forming part of a ribozyme expression vector of the invention. The cassette comprises the human placental TRNAval promoter (see AAF90356), with a 3' modification, and a DNA sequence corresponding to HIV-1 mRNA-targeted ribozyme TAR GUU Rz (see AAF90354). Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribozyme; constitutive transport element; virucide; gene therapy;
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                                                              63.3%; Score 85.4; DB 24; Length 137; 77.0%; Pred. No. 6.5e-20; tive 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "tRNAval with 3' modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA cassette for tRNAval-linked ribozyme TAR GUU Rz.
                      Sequence 137 BP; 33 A; 34 C; 34 G; 36 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Warashina M, Kuwabara T, Kawasaki H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92..131
/*tag= b
/note= "Tak GUU Rz"
147..151
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 13; 76pp; English.
                                                                                                                                                                                                                                                                                                                    121 GUCGGAAACGGUUUU 135
                                                                                                                                                                                                                                                                                                                                                              121 AACGUGAUGUUUUUU 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1; tRNAval; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF90357 standard; DNA; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-NOV-2000; 2000EP-0250368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                      104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens.
Chimeric - synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..91
/*tag=
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                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAIR/) TAIRA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1097993-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                terminator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF90357;
                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sliding
                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF9035;
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1 ACCGUUGGUUUCCGUAGUGUAGGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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molecules of the invention include ribozymes such as TAR GUU Rz linked to a constitutive transport element (see AAF90344), and expression vectors for such chimeric molecules. These are used in a claimed method to prevent or treat viral diseases, diseases associated with apoptosis or diseases associated with abnormal gene expression. They are also used in a claimed method of specifically cleaving a target nucleic acid, especially a viral gene, protooncogene or a gene associated with apoptosis. Use of the CTE facilitates cleaving of RNA previously considered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme; constitutive transport element; virucide; gene therapy; HIV-1; tRNAval; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                            ch 62.7%; Score 84.6; DB 22; Length 151; I Similarity 69.7%; Pred. No. 1.3e-19; 69; Conservative 21; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "constitutive transport element"
316..320
/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 UUCGAAACCGGGCACUACAACACACACGCGGUGAGGAC 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TTCGAAACCGGGCACTACAAAAACCAACTTTATCTGGTC 99
                                                                                                                                                                                                                                                                                                                                                                  Sequence 151 BP; 38 A; 39 C; 38 G; 36 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - synthetic.
Chimeric - Simian mason-pfizer type d retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Warashina M, Kuwabara T, Kawasaki H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INSC-) SEC AGENCY IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tRNAval-linked ribozyme TAR GUU Rz-CTE.
                                                                                                                                                                                                                                                                                                 refractory because of local structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=_ b
/note= "TAR GUU Rz"
138..309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF90358 standard; DNA; 320 BP
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Best Local Similarity
Matches 69; Conserv
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stem_loop
                                                                                                                                                                                                                stem_loop
          stem_loop
                                                                                                                                                                                                                                                                                                                                                         Taira K,
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                                                                                                                                                                                                                                                                          Nucleotide sequence of ribozyme useful as antiviral and gene expression
                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                      that can be used as antiviral and gene expression suppression agents. The ribozymes have high stability in vivo.
                                                                                                                                                                                              The invention provides nucleotide sequences of hammerhead ribozymes
                Sequence of a lower primer including Rz2 and terminator sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                            Ribozyme; ss; cytostatic; anti-HIV; ribozyme expression system; malignant disease; cancer; infectious disease; AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /bound_moiety= "tRNA-Luc GUA Rz ribozyme"
/note= "Binds nucleotides 88-81 of the tRNA-Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /bound_moiety= "tRNA-Luc GUA ribozyme"
/note= "Binds nucleotides 78-73 of the tRNA-Luc
22..32
                                                                                                                                                                                                                                           Query Match 63.3%; Score 85.4; DB 21; Length 109; Best Local Similarity 86.2%; Pred. No. 6.1e-20; Matches 75; Conservative 11; Mismatches 1; Indels 0;
                              Hammerhead ribozyme; antiviral; gene expression; primer; ss.
                                                                                                                                                                                                                             Sequence 109 BP; 18 A; 29 C; 30 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                          109 CGAAACGGGCACGUCGGAAACGGUUUU 135
                                                                                                                                                                                                                                                                                                                 49 CGAAACGGGCACGTCGGAAACGGTTT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                Examples; Page 16; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                               ABK51149 standard; RNA; 137 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rz Ribozyme"
                                                                                            98JP-0244755
                                                                                                           98JP-0244755
                                                                                                                           (AGEN ) KOGYO GIJUTSUINCHO.
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                             tRNA-Luc GUA Rz Ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRNA_Luc GUA Rz Ribozyme
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                                                                                                                                         WPI; 2000-075225/07
                                                                                                                                                                 suppression agents
                                                              JP2990268-B1.
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                                                                                            31-AUG-1998;
31-MAR-2000
                                                                                                           31-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2002
                                                                             13-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stem_loop
                                                                                                                                                                                                                                                                                                                                                                              ABK51149;
                                                                                                                                                                                                                                                                                                                                                 RESULT 7
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g
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This invention relates to a novel method for selecting a functional nucleic acid molecule functioning in a cell, cytoplasm or nucleus, comprising constructing an expression vector, introducing the expression vector into a cell, culturing the cell, collecting and preparing an extract of an entire cell, a cytoplasmic fraction or a nuclear fraction, incubacing the extract and obtaining a nucleic acid molecule. The invention also comprises a novel functional nucleic acid molecule which has an increased transcriptional level, stability or activity within cells or exhibits altered intracellular localisation, when compared to a corresponding control nucleic acid molecule. The method of the invention provides a means of obtaining highly functional nucleic acid molecules within cells which have high stability. Furthermore, a molecules within cells which have high stability. Furthermore, a corresponding or system with high efficiency can be developed, based on a linker sequence which a highly functional ribozyme has, and this expression system can be applied for treatment of malignant diseases such as cancers and infectious diseases including acquired immuno deficiency syndrome (AIDS). The present sequence represents the RNA sequence of the tRNA-Luc GUR Rz Ribozyme of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= j
/bound_moiety= "tRNA-Luc GUA Rz ribozyme"
/note= "Binds nucleotides 126 to 123 of the tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "tRNA-Luc GUA Rz Ribozyme"
/note= "Binds nucleotides 99-96 of the tRNA-Luc
                                                                                                                                                                                                                                                                                                                                                     /bound_moiety= "tRNA-Luc GUA Rz Ribozyme"
/note= "Binds nucleotides 19-14 of the tRNA-Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety= "tRNA-Luc GUA Rz Ribozyme"
/note= "Binds nucleotides 11-4 of the tRNA-Luc
                                                                                                                                                                                        f
"Optionally 22mer random sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rz Ribozyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rz Ribozyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-OCT-2001; 2001EP-0309183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-2000; 2000JP-0331347.
                                                                                                                                                                                                                                                                                                                                                                                                                        Rz Ribozyme"
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123..126
                                                     /*tag=
56..72
                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                               /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.
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                                                                                                                        /*tag=
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/*tag≃
                                                                                                                                                                                                                                                                                                                            /*tag=
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                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                        misc_binding
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                                                                                                                                                                                                                                                                                                                                                                                                             comprising a tetracyclin operator, at least one promotor and a DNA sequence emodding a ribozyme successively from the 5 'end. The tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from the transcription initiating site of the promotor. The expression cassette is useful in a method for preparing a cell having no sensitivity to HIV, and for inhibiting the growth of HIV. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 UUCGAAACCGGGCACUACAAACAC------AACACUGAUGAGGACCGAAAGGUCCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 ITCGAAACCGGGCACTACAAAACCAACGATTGGACTTCTGATGAGGACCGAAAGGTCCG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 88
                                                                                                                                                                                                                                                                                                         Ribozyme expression cassette, useful for preparing a cell insensitive to HIV and for inhibiting growth of HIV, comprises a tetracyclin operator, at least one promotor and a sequence encoding a ribozyme successively from the upstream side -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a ribozyme expression cassette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme; constitutive transport element; mouse; procaspase-3; CPP32; apoptosis; gene therapy; ss.
                                                          Nucleotide sequence of ribozyme expressing cassette, SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.2%; Score 89.4; DB 25; Length 175; 64.1%; Pred. No. 2.9e-21;
                                                                                Antiviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promotor; ribozyme; anti-HIV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse procaspase-3 mRNA targeted ribozyme CPP Rz5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 175 BP; 47 A; 39 C; 41 G; 48 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                                                                        KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 AAACGGGCACGUCGGAAACGGUUUU 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 AAACACTTGATTCCGGAAACGGTTT 173
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 16; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF90396 standard; RNA; 142 BP
                                                                                                                                                                                          09-MAR-2001; 2001JF-0067253.
                                                                                                                                                                                                                 09-MAR-2001; 2001JP-0067253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2001 (first entry)
                                 04-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93; Conservative
                                                                                                                                                                                                                                                                                      WPI; 2003-132124/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     TAKEBE Y
                                                                                                                                                                                                                                                                (OKAW/) OKAWA J.
                                                                                                                                          JP2002262880-A.
                                                                                                                                                                  17-SEP-2002
                                                                                                                    Synthetic.
           ABZ21216;
                                                                                                                                                                                                                                                    TAKE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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61 UUCGAAACCGGGCACUACAAACACAACACUGAUGAGGACCGAAAGGUCCGAAACGGCCAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel chimeric molecule useful for clarifying biological function of target nucleic acid and for treating viral diseases, and Alzheimer's disease, comprises region with binding affinity for molecule capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of novel ribozyme CPP Rz5, which is targeted to a stem-structured site site in mouse CPP32 mRNA that was previously considered inaccessible. CPP32 is an apoptosis-related encoding procaspase-3. CPP Rz3 was used to demonstrate the high efficacy of hybrid ribozymes linked to a constitutive transport element (CTB, See ARF30944) for inhibition gene expression. B Ribozymes for different sites in CPP32 mRNA were designed (see AAF90992-96). Mouse NIH3T3 cells were transfected with ribozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression plasmids and procaspace-3 expression levels were determined by Western blotting after 36 hr. CTE-linked ribozymes were more effective that their conventional counterparts for which they can be expression. The CTE moiety facilitates cleavage of RNA previously considered refractory because of local high-order structure. It binds to RNA helicase A, which has functions of binding to RNA, sliding and unwinding its high-order structure. Chimeric molecules of the invention, including treat viral diseases, diseases associated with apoptosis or diseases associated with apoptosis or diseases associated with apoptosis or are also used in a claimed method of specifically cleaving a target nucleic acid, especially a viral gene, protooncogene or a gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.7%; Score 87.4; DB 22; Length 142; 79.8%; Pred. No. 1.3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taira K, Warashina M, Kuwabara T, Kawasaki H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             (INSC-) SEC AGENCY IND SCI & TECHNOLOGY (TAIR/) TAIRA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 49; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ58601 standard; DNA; 109 BP.
                                                                                                                                                                                                                                                                                                   99JP-0316133.
                                                                                                                                                                                                                         03-NOV-2000; 2000EP-0250368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GUCGGAAAC 129
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                                                                                                                                                                                                                                                                                               05-NOV-1999;
                                                                     EP1097993-A2
                                                                                                                                                   09-MAY-2001
Synthetic.
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    UUCGAAACCGGGCACUACAAACACAACACGGAUGAGGACCGAAAGGUCCGAAACGGGCAC 120

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                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence of ribozyme useful as antiviral and gene expression
                                                                                                                                                                                                  1 ACCGUUGGUUUCCGGAGGGUGGGGGUAACCACGUCGCCCAAACGGCCCCGG
                                                                                                                                                                               1 ACCGUUGGUUUCCGUAGUGUAGUGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
The invention provides nucleotide sequences of hammerhead ribozymes that can be used as antiviral and gene expression suppression agents. The ribozymes have high stability in vivo. The present sequence represents an example of such a ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention provides nucleotide sequences of hammerhead ribozymes that can be used as antiviral and gene expression suppression agents. The ribozymes have high stability in vivo. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Gaps
                                                                                                                                                   Gaps
                                                                                                                                                ·
0
                                                                                                                  Length 136;
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                                                                                                                      , 4e-37;
10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammerhead ribozyme; antiviral; gene expression; ss.
                                                                                                             DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 142 BP; 39 A; 38 C; 37 G; 28 U; 0 other;
                                                                                 Sequence 136 BP; 36 A; 35 C; 37 G; 28 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of hammerhead ribozyme Rz3.
                                                                                                                                                0; Mismatches
                                                                                                               100.0%; Score 135; 100.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents an example of such a ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 1; 24pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ58591 standard; RNA; 142 BP
                                                                                                                                                                                                                                                                                                              GUCGGAAACGGUUUU 135
                                                                                                                                                                                                                                                                                                                                             121 GUCGGAAACGGUUUU 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000 (first entry)
                                                                                                                              al Similarity 100.
135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppression agents -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ58591;
                                                                                                                Query Match
Best Local 3
                                                                                                                                                 Matches
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The present invention relates to a ribozyme expression cassette comprising a tetracyclin operator, at least one promotor and a DNA sequence encoding a ribozyme successively from the 5' end. The tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from the transcription initiating site of the promotor. The expression cassette is useful in a method for preparing a cell having no sensitivity to HIV, and for inhibiting the growth of HIV. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 UUCGAAACCGGGCACUACAAACAC-----AACACUGAUGAGGACCGAAAGGUCCG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 ACCGTEGETTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ribozyme expression cassette, useful for preparing a cell insensitive to HTV and for inhibiting growth of HIV, comprises a tetracyclin operator, at least one promotor and a sequence encoding a ribozyme successively from the upstream side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.6%; Score 91.2; DB 25; Length 175; 69.2%; Pred. No. 6.8e-22; Ative 26; Mismatches 8; Indels 11;
                                                                                                                                                                                                                                 Nucleotide sequence of ribozyme expressing cassette, SEQ ID
                                                                                                                                                                                                                                                                  Antiviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promotor; ribozyme; anti-HIV; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 175 BP; 48 A; 40 C; 41 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AAAC-GGGCACGUCGGAAACGGUUUU 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AAACTTGACACTCCGGAAACGGTTTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 16; 27pp; Japanese.
115 GGGCACGUCGGAAACGGUUUU 135
                  121 GGGCACGUCGGAAACGGUUUU 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ21216 standard; DNA; 175 BP.
                                                                                                                         ABZ21217 standard; DNA; 175 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-2001; 2001JP-0067253.
                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAR-2001; 2001JP-0067253
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKEBE Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OKAW/) OKAWA J.
                                                                                                                                                                                                                                                                                                                                                       JP2002262880-A.
                                                                                                                                                                                               04-APR-2003
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                                                                                                                                                                                                                                                                                                                         Synthetic.
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ID ABZ2
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                                                                                         RESULT 3
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September 13, 2003, 08:06:21; Search time 195.652 Seconds (without alignments) 1862.612 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Nucleotide sequenc	Nucleotide sequenc	Nucleotide sequenc	Nucleotide sequenc	Mouse procaspase-3	Sequence of a lowe	tRNA-Luc GUA Rz Ri	DNA cassette for t
	ID	AAZ58590	AA258591	ABZ21217	AB221216	AAF90396	AAZ58601	ABK51149	AAF90357
	90	21	21	25	25	22	21	24	22
	Query Match Length DB ID	136	142	175	175	142	109	137	151
*	Query Match 1	100.0	88.1	9.79	66.2	64.7	63,3	63,3	62.7
	Score	135	119	91.2	89.4	87.4	85.4	85.4	84.6
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transval-linked rib Nucleotide sequenc Maxizyme related t Human RNA sequence Human RNA promote tet 01-transval seq Maxizyme related t Mouse procaspase-3 Mouse procaspase-3 Mouse procaspase-3 Mouse procaspase-3 Mouse procaspase-3 Mucleotide sequence Plasmid pBtV1-434 Plasmid pBtV1-434 Plasmid pZIP V1-43 Plasmid pZIP V1-43 Nucleotide sequence Nuc	of a mela mela mela mela mela mela mela me
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ALIGNMENTS

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Nucleotide sequence of ribozyme useful as antiviral and gene expression
                                                                                             Hammerhead ribozyme; antiviral; gene expression; ss.
                                                                         Nucleotide sequence of hammerhead ribozyme Rz2.
                                                                                                                                                                                                                                                                                   Claim 1; Page 1; 24pp; Japanese.
                 AAZ58590 standard; RNA; 136 BP.
                                                                                                                                                                          98JP-0244755.
                                                                                                                                                                                            98JP-0244755.
                                                                                                                                                                                                                (AGEN ) KOGYO GIJUTSUINCHO.
                                                       31-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                  suppression agents -
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                                                                                                                                                                          31-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of novel ribozyme CPP R22, which is targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related gene encoding procespase-3. CPP R22 was used to demonstrate the high efficacy of hybrid ribozymes linked to a constitutive transport clement (CTE, See AAR30944) for inhibition gene expression.

5 Ribozymes for different sites in CPP32 mRNA were designed (see expression plasmids and procespase-3 expression levels were expression plasmids and procespase-3 expression levels were certained by Western blotting after 36 hr. CTE-linked ribozymes were more effective that their conventional counterparts for inhibiting CPP32 gene expression. The CTE molety facilitates cleavage of RNA previously considered refractory because of local high-order structure. It binds to RNA helicase A, which has functions of binding to RNA, sliding and unwinding its high-order structure. Chimeric molecules of the invention, including cTE-ribozymes, and expression vectors, are used to prevent or treat viral diseases associated with apportosis or treat viral diseases associated with abnormal gene expression (claimed). They are also used in a claimed method of specifically cleaving a target not clear acid, sepecially a viral gene, protoncogene or a gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel chimeric molecule useful for clarifying biological function of target nucleic acid and for treating viral diseases, and Alzheimer's disease, comprises region with binding affinity for molecule capable of
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100.0%; Pred. No. 2.1e-18;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Taira K, Warashina M, Kuwabara T, Kawasaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INSC-) SEC AGENCY IND SCI & TECHNOLOGY. (TAIR/) TAIRA K.
CPP32; apoptosis; gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 47; 76pp; English.
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Matches 81; Conserva
                                                                                                                                                    EP1097993-A2
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                                                                          Synthetic.
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The present sequence is that of novel ribozyme CPP RZ3, which is targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related gene encoding procaspase-3. CPP RZ3 was used to demonstrate the high efficacy of hybrid ribozymes linked to a constitutive transport class in Ribozymes for different sites in CPP32 mRNA were designed (see SRibozymes for different sites in CPP32 mRNA were designed (see ARF90392-96). Mouse NHH3T3 cells were transfected with ribozymes conferencing and procaspase-3 expression levels were designed (see ARF90392-96). Mouse NHH3T3 cells were transfected with ribozymes conferencing and procaspase-3 expression levels were conferenced by western blotting after 36 hr. CTE-linked ribozymes conferenced for that their conventional counterparts for inhibiting CPP32 gene expression. The CTE moiety facilitates cleavage of RNA previously considered refractory because of local classage of RNA previously considered refractory because of local cluctions of binding to RNA, sliding and unwinding its high-order cructure. Chimeric molecules of the invention, including cructure. Chimeric molecules of the invention, including cructure cructure associated with approxis or treat viral diseases associated with approxis or diseases associated with abnormal gene expression (claimed). They can also used in a claimed method of specifically cleaving a triget of necessity and seed in a viral gene, protooncogene or a gene
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Ribozyme; constitutive transport element; mouse; procaspase-3; CPP32; apoptosis; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Taira K, Warashina M, Kuwabara T, Kawasaki H;
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(TAIR/) TAIRA K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleavage activity. More specifically the invention relates to anucleic acid enzyme, trans maxizyme, which has selective and effective eradicating activity towards harmful cells by acquiring cleavage activity of a specific target RNA by recognition of the other RNA molecule. The enzyme of the invention is useful for cleaving target RNA and is useful in treating diseases caused by the target RNA. This polynucleotide sequence represents the tRNA-val I-MzL sequence related to the maxizyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACCGUUGGUUCCGUAGUGUAGGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                        /*tag= g
//bound_moiety= "tRNA-val_T-MzL"
//note= "Forms a double-stranded region with nucleotides
11-4 of itself"
                                                                     /bound_moiety= "tRNA-val_T-MzL"
/note= "Forms a double-stranded region with nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A nucleic acid enzyme which has selective and effective eradicating activity towards harmful cells by acquiring cleavage activity of a specific target RNA by recognition of the other RNA molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid enzyme with modifiable RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ribozyme; constitutive transport element; mouse; procaspase-3; CPP32; apoptosis; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse procaspase-3 mRNA targeted ribozyme CPP Rz1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 138 BP; 31 A; 38 C; 32 G; 37 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.4%; Score 81; DB 24; I
100.0%; Pred. No. 2.1e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                           (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 7; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 UUCGAAACCGGGCACUACAAA 81
                                                                                                   19-14 of itself"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF90392 standard; RNA; 142 BP.
                                                                                                                                                                                                                                                                                                                                                              13-0CT-2000; 2000JP-0313320.
                                                                                                                                                                                                                                                                                                                               13-OCT-2000; 2000JP-0313320.
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111..128
/*tag= i
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/*tag=
56..72
                         /*tag=
                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-483792/52.
                                                                                                                                                                                                                                                                       JP2002119283-A.
                                                                                                                  misc_binding
                                         misc_binding
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              stem_loop
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The present sequence is that of novel ribozyme CPP Rz1, which is targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related gene encoding processpase-3. CPP Rz1 was used to demonstrate the high efficacy of hybrid ribozymes linked to a constitutive transport clement (CTE, See AAF30944) for inhibition gene expression.

5. Ribozymes for different sites in CPP3 mRNA were designed (see AAF90329-96). Mouse NUH373 cells were transfected with ribozyme caternined by Western blotting after 36 hr. CTE-linked inbozymes were more effective that their conventional counterparts for inhibiting CPP32 gene expression. The CTE moiety facilitates cleavage of RNA previously considered refractory because of local high-order structure. It binds to RNA helicase A, which has functions of binding to RNA, sliding and unwinding its high-order structure. Chimeric molecules of the invention, including cTE-ribozymes, and expression vectors, are used to prevent or diseases associated with abnormal gene expression (claimed). They are also used in a claimed method of specifically cleaving a target associated with apoptosis.
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                                                                                                                                                                                                                                                                                                              Novel chimeric molecule useful for clarifying biological function of target nucleic acid and for treating viral diseases, and Alzheimer's disease, comprises region with binding affinity for molecule capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozyme; constitutive transport element; mouse; procaspase-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse procaspase-3 mRNA targeted ribozyme CPP Rz2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 142 BP; 36 A; 42 C; 37 G; 27 U; 0 other;
                                                                                                                                                                                                                                              Taira K, Warashina M, Kuwabara T, Kawasaki H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57.4%; Scor.
100.0%; Pred. No. z...
                                                                                                                                                                                          (INSC-) SEC AGENCY IND SCI & TECHNOLOGY.
(TAIR/) TAIRA K.
                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 47; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 UUCGAAACCGGGCACUACAAA 81
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                                                                                                                                                        99JP-0316133,
                                                                                                                      03-NOV-2000; 2000EP-0250368.
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                                                                                                                                                                                                                                                                              WPI; 2001-357832/38.
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                                                                                                                                                      05-NOV-1999;
                                                EP1097993-A2
                                                                                  09-MAY-2001.
               Synthetic
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                                                                                                                                                                                                                                                                                                                                                      Ribozyme, ss; cytostatic; anti-HIV; ribozyme expression system, malignant disease; cancer; infectious disease; AIDS; acquired immunodeficiency syndrome; human immunodeficiency virus; tRNA_Luc GUA Rz Ribozyme.
                                                                                                                                                                                                                                                                                                                                                                               /bound_moiety= "tRNA-Luc GUA Rz ribozyme"
/note= "Binds nucleotides 126 to 123 of the tRNA"
                                                                                                                                                                   /*tag= b
/bound_moiety= "tRNA-Luc GUA ribozyme"
/note= "Binds nucleotides 78-73 of the tRNA-Luc
                                                                                                                                      /bound_moiety= "tRNA-Luc GUA Rz ribozyme"
/note= "Binds nucleotides 88-81 of the tRNA-Luc
                                                                                                                                                                                                                                                                                    /bound_molety= "tRNA-Luc GUA Rz Ribozyme"
/note= "Binds nucleotides 19-14 of the tRNA-Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                  /bound_moiety= "tRNA-Luc GUA Rz Ribozyme"
/note= "Binds nucleotides 99-96 of the tRNA-Luc
Rz Ribozyme"
                                                                                                                                                                                                                                                                                                                        /bound_molety= "tRNA-Luc GUA Rz Ribozyme"
/note= "Binds nucleotides 11-4 of the tRNA-Luc
                                                                                                                                                                                                                                                       /note= "Optionally 22mer random sequence nonnnonnonnonnonnonnonnonnonnonnon
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/note= "Ribozyme region"
                                                                                                                  Location/Qualifiers
       ABK51149 standard; RNA; 137 BP
                                                                                                                                                      Rz Ribozyme"
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                                    (first entry)
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                                                  tRNA-Luc GUA Rz Ribozyme.
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34..50
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56..72
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70..91
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                                                                                                                 Key
misc_binding
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                                                                                                   Synthetic
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ABK51149
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This invention relates to a novel method for selecting a functional nucleic acid molecule functioning in a cell, cytoplasm or nucleus, comprising constructing an expression vector, introducing the expression vector into a cell, culturing the cell, collecting and preparing an extract of an entire cell, a cytoplasmic fraction or a nuclear fraction, incubating the extract and obtaining a nucleic acid molecule. The invention also comprises a novel functional nucleic acid molecule which has an increased transcriptional level, stability or activity within cells or exhibits altered intracellular localisation, when compared to a corresponding control nucleic acid molecule. The method of the invention provides a means of obtaining highly functional nucleic acid molecules within cells which have high stability. Furthermore, a notence expression system with high efficiency can be developed, based on a linker sequence which a highly functional ribozyme has, and this expression system can be applied for treatment of malignant diseases such as cancers and infectious diseases including acquired immuno deficiency syndrome (AIDS). The present sequence represents the RNA sequence of the tRNA-Luc GUA RZ Ribozyme of the invention.
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/hote= "Forms a double-stranded region with nucleotides
78-73 of itself"
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                                                                                                                  Selecting a functional nucleic acid molecule functioning in a cell, cytoplasm or nucleus using an expression vector which contains a candidate nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 137;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.4%; Score 81; DB 24; I
100.0%; Pred. No. 2.1e-18;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                  Example 1; Figure 2a; 17pp; English.
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/*tag=
34..50
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                                                         WPI; 2002-428565/46
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   Sano M;
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misc_binding
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Taira K,
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AAL40467
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                                                                                                                                                                        1 ACCGUUGGUUUCCGUAGUGGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                              Human; maxizyme; target mRNA; helicase activity; viral disease; human immunodeficiency virus; HIV; hepatitis C; hepatitis B; cancer; apoptosis-associated disease; Alzheimer's disease; Parkinson's disease; autoimmune disease; inflammatory disease; genetic disorder; mRNA cleavage; virucide; nookropic; antiparkinsonian; cytostatic; antiinflammatory; immunosuppressive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a novel maxizyme that can bind to a target mRNA molecule or a molecule having helicase activity. The maxizyme is useful for the prevention and treatment of viral diseases such as human immunodeficiency virus (HIV), hepatitis C or hepatitis B, apoptosis-associated diseases such as Alzheimer's and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maxizyme binding to a molecule with helicase activity for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           irrespective of the higher-order structure of the latter. The present sequence represents a human RNA sequence relating to the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hara T, Nozawa I;
sequence represents the tRNA-val promoter sequence relating to the maxizyme enzyme of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases, cancer, autoimmune diseases, inflammatory diseases and genetic disorders. The maxizyme binds to and cleaves target mRNA
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0
                                                                                              Length 88;
                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taira K, Warashina T, Warashina M, Kawasaki H,
                                                                                            57.4%; Score 81; DB 24; L
100.0%; Pred. No. 1.9e-18;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
                                                          Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human RNA sequence relating to novel maxizyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection cancer and autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 30-31; 36pp; Japanese.
                                                                                                                                                                                                                                                 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                     61 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                                                                                                                 ABX12785 standard; RNA; 88 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2001; 2001JP-0134469.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-APR-2002; 2002WO-JF04322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIS ) TAISHO PHARM CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                1 Similarity 100.
81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) GENOFUNCTION INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-129298/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200292821-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-NOV-2002.
                                                                                                                                                                                                                                                 61
                                                                                              Query Match
                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising a tetracyclin operator, at least one promotor and a DNA sequence encoding a ribozyme successively from the 5' end. The tetracyclin operator is present at 2 to 0 nucleotides to 5'-end from the transcription initiating site of the promotor. The expression assette is useful in a method for preparing a cell having no sensitivity to HTV, and for inhibiting the growth of HTV. To illustrate the invention, a tet 01-human tRNAVal promoter cassette was constructed,
                                                                                                         09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                       9
                                                                                  1 ACCGUUGGUUCCCGUAGUGUAGUGGUAACACGUUCGCCCAAAACGUCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribozyme expression cassette, useful for preparing a cell insensitive to HTV and for inhibiting growth of HTV, comprises a tetracyclin operator, at least one promotor and a sequence encoding a ribozyme successively from the upstream side -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 ACCGTIGGTITCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG
                                                    1 ACCGUUGGUUUCCGUAGUGUAGGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a ribozyme expression cassette
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  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antiviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promotor; ribozyme; anti-HIV; ds.
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  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tet 01-tRNAVal sequence, SEQ ID 1.
                                                                                                                                                                 61 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                      61 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 15; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                              ABZ21212 standard; DNA; 117 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAR-2001; 2001JP-0067253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2001; 2001JP-0067253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-132124/13.
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es 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OKAWA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP2002262880-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                   ABZ21212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                         RESULT 10
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11

RESULT

Length 88;

57.4%; Score 81; DB 25; 1 100.0%; Pred. No. 1.9e-18;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACCGUGGUUUCCGUAGUGGUAGUGGUAAUCACGUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ACCGUUGGUUUCCGUAGUGUAGUGUAACACGUUAACACACGCGAAAGGUCCCCGG 60
disease, comprises region with binding affinity for molecule capable of sliding \, -
                                                                                        The present sequence is that of novel ribozyme CPP R23, which is targeted to a site in mouse CPP32 mRNA. CPP32 is an apoptosis-related gene encoding procespase-3. CPP R23 was used to demonstrate the high efficacy of hybrid ribozymes linked to a constitutive transport element (CTE, See AAR70944) for inhibition gene expression. S Ribozymes for different sites in CPP32 mRNA were designed (see AAR70329595). Mouse NH373 cells were transfected with ribozyme expression plasmids and procespase-3 expression levels were determined by Western blotting after 36 hr. CTE-linked ribozymes were more effective that their conventional counterparts for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               diseases associated with abnormal gene expression (claimed). They are also used in a claimed method of specifically cleaving a target nucleic acid, especially a viral gene, protooncogene or a gene
                                                                                                                                                                                                                                                                              inhibiting CPP32 gene expression. The CTE moiety facilitates cleavage of RNA previously considered refractory because of local high-order structure. It binds to RNA helicase A, which has functions of binding to RNA, sliding and unwinding its high-order structure. Chimeric molecules of the invention, including CTE-ribozymes, and expression vectors, are used to prevent or treat viral diseases, diseases associated with apoptosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid enzyme; maxizyme; allosteric RNA-cleaving activity; RNA cleavage; chronic myeloid leukemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%; Score 82.6; DB 22; Length 141; 80.2%; Pred. No. 5.9e-19; 1.1ve 0; Mismatches 24; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 141 BP; 37 A; 37 C; 35 G; 32 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA cleavage; chronic myeloid leukemia;
Philadelphia chromosome abnormality; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAIS ) TAISHO PHARM CO LTD.
(AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
                                                           Example 1; Page 48; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of tRNA-val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ10600 standard; RNA; 88 BP.
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98JP-0311098.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associated with apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.2'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ACCGUUGGUUCCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCGUUGGUUUCCGUAGUGUAAGGGUUAUCACGUUACGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                             RNA-cleaving activity, used for
                                                                                                                                                                                                                The maxizyme
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enzyme; modifiable RNA cleavage activity; maxizyme-constituting RNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A nucleic acid enzyme which has selective and effective eradicating activity towards harmful cells by acquiring cleavage activity of a specific target RNA by recognition of the other RNA molecule \cdot
                                                                                                                                                                                                            left and right arms of a nucleic acid enzyme (maxizyme). The maxizy has allosteric RNA-cleaving activity on a specific target RNA. The maxizyme can be used for efficient cleavage of RNA molecules at specific points, especially for the prevention and treatment of chronic myeloid leukemia and Philadelphia chromosome abnormality. The present sequence is used in the course of the invention.
                                                                                                                                                                                           The specification describes nucleotide sequences which make up the
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0
                                                                                                                                                                                                                                                                                                                                                                                           Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 57.4%; Score 81; DB 20; I Best Local Similarity 100.0%; Pred. No. 1.9e-18; Matches 81; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                   Sequence 88 BP; 23 A; 25 C; 21 G; 19 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maxizyme related tRNA-val promoter sequence.
                                                                                           Nucleic acid enzyme having allosteric treatment of chronic myeloid leukemia
                  Hitoshio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 UUCGAAACCGGGCACUACAAA 81
                                                                                                                                                        Claim 8; Page 55; 93pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 2; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAL40450 standard; tRNA; 88 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trans maxizyme; tRNA-val; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-OCT-2000; 2000JP-0313320
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                Kuwabara T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-483792/52,
                                                      WPI; 1999-551415/46.
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                  Taira K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAL40450;
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WPI; 2001-357832/38.
                                                                                                                                        WPI; 2001-373027/39.
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hes 68; Conserv
                     JP2001128682-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1999;
Homo sapiens.
                                                                                           05-NOV-1999;
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                                                                   05-NOV-1999;
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                                             15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE90395;
                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                            Matches
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δŏ
                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a ribozyme expression cassette comprising a tetracyclin operator, at least one promotor and a DNA sequence encoding a ribozyme successively from the 5' end. The tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from the transcription intitiating site of the promotor. The expression cassette is useful in a method for preparing a cell having no sensitivity to HIV, and for inhibiting the growth of HIV. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 UUCGAAACCGGGCACUACAAACCAACAC----ACAACACUGAUGAGGACCGAAAGGUCCG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 ITCGAAACCGGGCACTACAAAAACCAACGATTGGACTTCTGATGAGGACCGAAAGGTCCG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 ACCGTIGGTITCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGAAAGGTCCCCGG 88
                                                                                                                                                                                                                                                                                                           Ribozyme expression cassette, useful for preparing a cell insensitive to HIV and for inhibiting growth of HIV, comprises a tetracyclin operator, at least one promotor and a sequence encoding a ribozyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                          Nucleotide sequence of ribozyme expressing cassette, SEQ ID 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 65.1%; Score 91.8; DB 25; Length 175; l. Similarity 64.1%; Pred. No. 4e-22; 93; Conservative 26; Mismatches 22; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Ribozyme; hammerhead type ribozyme; p16; cancer; ss.
                                                                                Antiviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promotor; ribozyme; anti-HIV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 175 BP; 47 A; 39 C; 41 G; 48 T; 0 other;
                                                                                                                                                                                                                                         (KOKU-) KOKURITSU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AAACGGCACGUCGGAAACGGUUUU 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AAACACTTGATTCCGGAAACGGTTT 173
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 16; 27pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                 successively from the upstream side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH47825 standard; DNA; 100 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human tRNA promoter sequence.
                                                                                                                                                                                         09-MAR-2001; 2001JP-0067253
                                                                                                                                                                                                                  09-MAR-2001; 2001JP-0067253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-SEP-2001 (first entry)
                                  04-APR-2003 (first entry)
                                                                                                                                                                                                                                                                                      WPI; 2003-132124/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     (TAKE/) TAKEBE Y.
(OKAW/) OKAWA J.
                                                                                                                                           JP2002262880-A.
                                                                                                                                                                   17-SEP-2002.
                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH47825;
           ABZ21216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel chimeric molecule useful for clarifying biological function of target nucleic acid and for treating viral diseases, and Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribozyme; constitutive transport element; mouse; procaspase-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.0%; Score 83.2; DB 22; Length 100; 70.8%; Pred. No. 3.3e-19; tive 20; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse procaspase-3 mRNA targeted ribozyme CPP Rz4.
                                                             (KEIZ-) KEIZAI SANGYOSHO SANGYO GLJUTSU SOGO KEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 100 BP; 30 A; 25 C; 21 G; 24 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 UUCGAAACCGGGCACUACAAACCAACACACACACU 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taira K, Warashina M, Kuwabara T, Kawasaki H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INSC-) SEC AGENCY IND SCI & TECHNOLOGY. (TAIR/) TAIRA K.
                                                                                                                                                                                                        A screening method for active ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPP32; apoptosis; gene therapy; ss.
                                                                                                                                                                                                                                                                         Example 1; Page 3; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-2000; 2000EP-0250368.
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99JP-0314579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF90395 standard; RNA; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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ABZ21216 standard; DNA; 175 BP.
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ID AB22
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                    93
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                                                                                                                                                                                                                                                          61 UUCGAAACCGGGCACUACAA-----ACACAACACUGAUGAGGACGGAAAGGUCGGAAAC 114
                                                                                                                                                                                                                                         61 UUCGAAACCGGGCACUACAAACCAACACACAACACUGAUGAGGACCGAAAGGUCCGAAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCGUUGGUUUCCGUAGUGGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ACCGUGGGUUCCGUAGUGUAGGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                             9
                                                                                                                                                                                             Nucleotide sequence of ribozyme useful as antiviral and gene expression
                                                                                                                                                                             1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides nucleotide sequences of hammerhead ribozymes that can be used as antivixal and gene expression suppression agents. The ribozymes have high stability in vivo. The present sequence represents an example of such a ribozyme.
The invention provides nucleotide sequences of hammerhead ribozymes that can be used as antiviral and gene expression suppression agents. The ribozymes have high stability in vivo. The present sequence represents an example of such a ribozyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Gaps
                                                                                                                                              Gaps
                                                                                                                                             0;
                                                                                              100.0%; Score 141; DB 21; Length 142; larity 100.0%; Pred. No. 3.1e-39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.4%; Score 119; DB 21; Length 136; 95.7%; Pred. No. 1.3e-31; ive 0; Mismatches 0; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hammerhead ribozyme; antiviral; gene expression; ss.
                                                                                Sequence 142 BP; 39 A; 38 C; 37 G; 28 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 136 BP; 36 A; 35 C; 37 G; 28 U; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of hammerhead ribozyme Rz2.
                                                                                                                                                                                                                                                                                                                                  121 GGGCACGUCGGAAACGGUUUU 141
                                                                                                                                                                                                                                                                                                    121 GGGCACGUCGGAAACGGUUUU 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 1; 24pp; Japanese,
                                                                                                                                                                                                                                                                                                                                                                                                              AAZ58590 standard; RNA; 136 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.7'
Matches 135; Conservative
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                                                                                                                              Similarity
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                                                                                                                            Best_Local Simi
Matches 141;
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                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
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The present invention relates to a ribozyme expression cassette comprising a tetracyclin operator, at least one promotor and a DNA sequence encoding a ribozyme successively from the 5' end. The tetracyclin operator is present at 2 to 10 nucleotides to 5'-end from the transcription initiating site of the promotor. The expression cassette is useful in a method for preparing a cell having no sensitivity to HIV, and for inhibiting the growth of HIV. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 UUCGAAACCGGGCACUACAAA----CCAACACACAACACUGAUGAGGACCGAAAGGUCCG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 ACCGTTGGTTTCCGTAGTGTAGTGGTTATCACGTTCGCCTAACACGCGGAAAGGTCCCCGG 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ribozyme expression cassette, useful for preparing a cell insensitive to HTV and for inhibiting growth of HTV, comprises a tetracyclin operator, at least one promotor and a sequence encoding a ribozyme successively from the upstream side -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACCGUUGGUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of ribozyme expressing cassette, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antlviral; gene therapy; ribozyme expression cassette; tetracyclin operator; promotor; ribozyme; anti-HIV; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 175 BP; 48 A; 40 C; 41 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 AAAC-GGGCACGUCGGAAACGGUUUU 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KOKU-) KOKURIISU YOBO EISEI KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 16; 27pp; Japanese.
                                  115 GGGCACGUCGGAAACGGUUUU 135
121 GGGCACGUCGGAAACGGUUUU 141
                                                                                                                                                                                                                                                 AB221217 standard; DNA; 175 BP
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKEBE Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (OKAW/) OKAWA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2002262880-A.
                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2003
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Nucleotide sequenc
Nucleotide sequenc
Nucleotide sequenc
Rucleotide sequenc
Human tRNA promote
Mouse procaspase-3
                                                                                                                                                         (without alignments)
1862.612 Million cell updates/sec
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                                                                                                                                   September 13, 2003, 08:06:21; Search time 204.348 Seconds
                                                                                                                                                                                                                                                 141
1 accguugguuuccguagugu.....ggcacgucggaaacgguuu 141
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%IDE1/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT:*
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/SIDS1/gcgdata/geneseqr.emb1/NA1984.DAT:*
/SIDS1/gcgdata/geneseqr.emb1/NA1984.DAT:*
/SIDS1/gcgdata/geneseqr.emb1/NA1986.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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AAZ58590
ABZ21217
ABZ21216
AAH47825
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AAZ10600
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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ALIGNMENTS

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Nucleotide sequence of ribozyme useful as antiviral and gene expression
                                                                                    Hammerhead ribozyme; antiviral; gene expression; ss
                                                                  Nucleotide sequence of hammerhead ribozyme Rz3.
                AAZ58591 standard; RNA; 142 BP.
                                                                                                                                                          98JP-0244755.
                                                                                                                                                                          98JP-0244755
                                                                                                                                                                                            (AGEN ) KOGYO GIJUTSUINCHO.
                                                 31-MAR-2000 (first entry)
                                                                                                                                                                                                             WPI; 2000-075225/07.
                                                                                                                                                                                                                                         suppression agents
                                                                                                                                                          31-AUG-1998;
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                                                                                                                      JP2990268-B1
                                                                                                                                        13-DEC-1999
                                                                                                     Synthetic.
                                 AAZ58591;
RESULT 1
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Claim 1; Page 1; 24pp; Japanese

Maxizyme related t Nucleotide sequenc

Query Match

57.4%; Score 81; DB 6; Length 88;

Best Local Similarity 76.5%; Pred. No. 8.3e-13;

Matches 62; Conservative 19; Mismatches 0; Indels BASE COUNT ORIGIN δy Q

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19 t

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23 a

Search completed: September 13, 2003, 10:39:39 Job time: 1436.54 secs

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AX453846.1 GI:21713515
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Best Local Similarity
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                                                                                                                1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                Tachi,C., Nakamaura,K., Horii,T., Murata,C., Nishimura,S.,
Nishino,K., Nakayama,A. and Talra,K.
Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
Unpublished
                                                                                                                               ABO80624 153 bp DNA linear SYN 21-MAY-
Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.0%; Score 81.8; DB 12; Length 153; 75.3%; Pred. No. 4.6e-13; live 19; Mismatches 2; Indels 0;
                                                      ; Score 81.8; DB 12; Length 153;
; Pred. No. 4.6e-13;
19; Mismatches 2; Indels 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/note="derived from ribozyme"
40 a 38 t
/note="derived from ribozyme" 35 c 39 g 43 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description of Artificial Sequence: tRNAVal promoter sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                             Nucleic acid enzymes acquiring an activity for cleaving a target rna by recognising another molecule Patent: EP 1213351-A 5 12-JUN-2002;
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JP 2002119283-A/5
JP 2002119283-B
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JP 2000313320
KAZUNARI TAIRA,MASAKI WARASHINA, FOC
                                                                                                                                                                                                                                                                                                                                                                                                                             57.4%; Score 81; DB 6; Length 88; 76.5%; Pred. No. 8.3e-13; ative 19; Mismatches 0; Indels
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25 c 21 g 19 t
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/mol_type="mRNA"
/db_xref="taxon:32630"
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1 (bases 1 to 88)
Taira,K., Warashina,M. and Warashina,T.
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                                                                                          Taira, K., Warashina, M. and Warashina, T.
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                                               artificial sequences.
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/note="derived from tRNA"
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                                              Tachi, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of Veterinary Medicine, Lab. Developmental and Reproductive Biotechnology; 1-17-71, Fuchinobe, Sagamihara-shi 229-8501, Japan (E-mail:tachi@azabu-u-ac.jp, Tel:81-3-3997-2757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ACCGUUGGUUUCCGUAGUGUAAGGGUUAUCACGUUACCCCUAACACGCGAAAGGUCCCCGG 60
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                                                                                                                                                                                                                                                                                                                            Nishino,K., Nakayama,A. and Taira,K. Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABO80622 153 bp DNA linear SYN 21-MAY-
Synthetic construct DNA for tRNAYal/anti-mSry ribozyme complex
                                                                                                                                                   AB080621 153 bp DNA linear SYN 21-MAY
Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
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                                                                                                                                                                                                                                                                                                                     Pachi,C., Nakamaura,K., Horii,T., Murata,C., Nishimura,S.,
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/note="derived from tRNA"
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Direct Submission
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SYN 21-MAY-2003
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                                                                                          Direct Submission
Submitted (27-FEB-2002) Chikashi Tachi, Azabu University School of
Veterinary Medicine, Lab. Developmental and Reproductive
Biotechnology; 1-17-71, Fuchinobe, Sagamihara-shi 229-8501, Japan (E-mail:tachi@azabu-u.ac.jp, Tel:81-3-3997-2757)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCCUAACACACGCGAAAGGUCCCCGG 60
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Nishino,K., Nakayama,A. and Taira,K.
Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
Onpublished
Cleavage of murine Sry mRNA by anti-mSry tRNA/ribozyme complexes
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Synthetic construct DNA for tRNAval/anti-mSry ribozyme complex
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/product="tRNAval/anti-mSry ribozyme complex
anti-mSrytRNA/Rz2"
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1. .87
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/organism="synthetic construct"
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/note="derived from ribozyme"
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/function="anti murine Sry ribozyme"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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    /note="derived from tRNA"

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/note="derived from tRNA"
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artificial sequences.

1 (Dases I to 141)

Taira,K., Warashina,M., Kuwabara,T. and Kawasaki,H.
Slidable functional chimeric molecule
Patent: JP 2001190282-A 52 I7-UUL-2001;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL
SCIENCE AND MANABU NAKAJIMA TECHNOLOGY, KAZUNARI TAIRA
                                                                                                                           Artificial Sequence
JP 2001190282-A/52
17-JUL-2001
02-NOY-2000 JP 2000336082
KAZUNARI TAIRA,MASAKI WARASHINA,TOMOKO KUWABARA,HIROAKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 82.6; DB 6; Length 141; 63.6%; Pred. No. 2.7e-13; tive 20; Mismatches 24; Indels (
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/organism='Artificial Sequence'.
Location/Qualifiers
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63.6%; File
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SYN 21-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACCEUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG
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/product="tRNAval/anti-mSry ribozyme complex
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JP 2001190282-A/52.
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Best Local Similarity 63.6%
Matches 77; Conservative
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                                                                                                                                                                                                                                                              Best Local Similarity 70.8 Matches 68; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                Ribozyme expression system Patent: JP 2002262880-a 5 17-SEP-2002; DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
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C12N15/09,C12Q1/68//C12N5/10,C12N15/00,C12N5/00 CC
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Location/Qualifiers
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PD 17-SEP-2002
PP 19-SEP-2002
PP 19-MAR-2001 JP 2001067253
PF 19-MAR-2001 JP 2001067253
PF 19-MAR-2001 JP 2001067253
PF 19-MAR-2001 JP 2001067253
PF 109-MAR-2001 JP 2001067253
PC 12N15/09, A61K31/711, A61K35/76, A61K48/00, A10K15/00, C12N15/00, C12N
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//organism="synthetic construct"
//mol_type="genomic DNA"
/db_xref="taxon:32630"
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05-NOV-1999 JP 1999314579
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Tabira, K. and Kawasaki, H.
BD174679.1 G1:29120369
TP 2002262880-A/5.
synthetic construct
synthetic construct
artificial sequences.
1 (Dases 1 to 175)
Takebe,Y. and Okawa,J.
                                                                                                                                                                                                                                                            YUTAKA TAKEBE, JUN OKAWA
OS Artificial Sequence
PN JP 2002262880-A/5
PD 17-SEP-2002
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JP 2001128682-A/9.
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                                                                                                                                                                             ·;
                                                                                                                               59.0%; Score 83.2; DB 6; Length 100; 70.8%; Pred. No. 1.9e-13; Live 20; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%; Score 82.6; DB 6; Length 141; 63.6%; Pred. No. 2.7e-13; tive 20; Mismatches 24; Indels (
                                                                                                                                        1.9e-13;
-hac 8; Indels
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/mol_type="mRNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52 from Patent EP1097993. AX138491
/organism="Homo sapiens"
                       /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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BD174680
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Tabira,K., Okawa,A. and Ozeki,S.
Expression system for functional nucleic acid transcription
Patent: Up 2000069972-A 1 07-MAR-2000;
AGENCY OF IND SCIENCE & TECHNOL
OS Artificial Sequence
PN JP 2000069972-A/1
PD 07-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E33203 130 136 bp RNA linear PAT 31-3
Expression system for functional nucleic acid transcription.
                                                             KAZUNARI TABIRA, ATSUSHI OKAWA, SHIORI OZEKI
C12N15/09, A61K31/70, A61K35/76, A61K48/00, C12N15/00 CC
Key
Location/Qualifiers
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/mol_type="genomic RNA"
/db_xref="taxon:32630"
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/mol_type="genomic RNR"
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1 (bases 1 to 136)
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JP 2000069972-A/1.
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PAT 18-MAR-2003
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                                                          61 UUCGAAACCGGGCACUACAAACCAACACAACACUGAUGAGGACGGAAAGGUCGGAAAC 120
                                                                                61 UUCGAAACCGGGCACUACAAA----CCAACACACACACACUGAUGAGGACCGAAAGGUCCG 116
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1 ACCGUUGGUUUCCGUAGUGAAGAGAUAACACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YUTAKA TAKEBE, JUN OKAWA
C12N15/09, A61K31/711, A61K35/76, A61K48/00, A61P31/18, C12N5/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribozyme expression system Patent: JP 2002262880-A 6 17-SEP-2002; DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIONS DISEASES,
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/mol_type="genomic DNA"
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OS Artificial Sequence
PN JP 2002262880-A/6
PD 17-SEP-2002
PF 09-MAR-2001 JP 2001067253
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1 (bases 1 to 175)
Takebe, Y. and Okawa, J.
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments)
4018.170 Million cell updates/sec
                 September 13, 2003, 09:38:16; Search time 1435.54 Seconds
                                                     US-09-763-590-2
141
1 accguugguuuccguagugu.....ggcacgucggaaacgguuuu 141
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Maximum Match 100%
Listing first 45 summaries
OM nucleic - nucleic search, using sw model
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	B33204 Expression B33203 Expression BD174679 Ribozyme BD174679 Ribozyme BA7138491 Sequence BD015659 Slidable AB080621 Synthetic AB080621 Synthetic AB080622 Synthetic AB080622 Synthetic AB080622 Synthetic AB080622 Synthetic AB080623 Synthetic AB080623 Synthetic AB080623 Synthetic AB080624 Synthetic AB080624 Synthetic AB080625 Synthetic AB080625 Synthetic AB080625 Synthetic AB080625 Synthetic AB080626 Synthetic AB080626 Synthetic AB18236 Novel max BD14350 Novel max BD14350 Novel max BD14350 Novel max BD14350 Novel max AX13849 Sequence AX13849 Sequence AX13849 Sequence AX13849 Sequence AX13849 Sequence AX13845 Sequence BD015656 Slidable BD015656 Slidable BD015656 Slidable BD015657 Slidable BD01567 Slidable BD015660 Slidable BD015617 Slidable BD015617 Slidable BD015617 Slidable BD015618 Slidable BJ3207 Expression BJ3207 Expression BJ3207 Expression BJ3207 Expression BJ3207 Expression BJ3207 Expression BJ3208 Supplession BJ3208 Supples	RNA linear PAT 31-JAN-2002 nucleic acid transcription nucleic acid transcription 2000;
SUMMARIES 3 ID	6 E33204 6 E33204 6 E33203 6 E34714 6 MAI38491 6 MAI38491 12 AB080621 12 AB080622 12 AB080622 12 AB080623 12 AB080623 12 AB080624 6 BD143502 6 BD143502 6 BD143502 6 BD143502 6 BD143601 6 AXI38490 6 BD15659 6 BD015659 6 BD015659 6 BD015659 6 BD015659 6 BD015659 6 BD015617 6 AXI38447 6 AXI38447 6 AXI38447 6 BD015618 6 BD015618 7 AXI38447 6 AXI38447 6 AXI38447 6 AXI38447 6 AXI38447 6 BD015618 6 BD015618 6 BD015618	ALLUMENT 142 bp r functional 8 and Ozeki,S. r functional 2-A 2 07-MAR- E & TECHNOL
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Result	0 0	RESULT 1 E33204 LOCUS DEFINITION ACCESION VERSION VERSION KEYWORDS SOURCE OURCE OURCA AUTHORS TITLE JOURNAL

91 GGTTTCTATGGTGTAGTMGTTACCACGCTGGCCTAACACATGGAAGGTCCTCTATTTGAA 150 рр

67 AC 68 || |151 AC 152

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Search completed: September 13, 2003, 09:43:48 Job time : 164.75 secs

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RESULT 14
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TITLE OF INVENTION: MCSQUITO OLFACTORY GENES, POLYPEPTIDES, AND METHODS OF

TITLE OF INVENTION: USE THEREOF

FILE PEFERENCE: N7841

CURRENT APPLICATION NUMBER: US/10/056,405

CURRENT FILING DATE: 2002-01-24

PRIOR FILING DATE: 2001-01-26

NUMBER OF SEQ ID NOS: 23

SOFTWARE: PATCHIN VET: 2.1

SEQ ID NO 23

LENGTH: 11103
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                                                                                                                                                                                           APPLICANT: Huang, Tim

IIILE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
FILLE REPERENCE: UND1523
CURRENT APPLICATION NUMBER: US/10/081,327
CURRENT FILING DATE: 2002-02-1
PRIOR APPLICATION NUMBER: 06/120,592
PRIOR APPLICATION NUMBER: 06/118,760
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.0
SEQ ID NO 32
LENGIH: 118067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Sequence 23, Application US/10056405; Publication No. US20030166013A1; GENERAL INFORMATION:
                                                                                                          US-10-081-327-32
, Sequence 32, Application US/10081327
; Publication No. US20030129602A1
; GENERAL INFORMATION:
                 763 TGGGTGAAAACATA 750
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Best Local Similarity 53.8
Matches 56; Conservative
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US-10-056-405-23
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US-10-056-405-23
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                                                                                           APPLICANT: ZWIEBEL, LAURENCE J.

TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
FILE REFRENCE: N9829
CURRENT APPLICATION NUMBER: US/10/094,240
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION WUMBER: 10/056,405
PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
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Sequence 272410, Application US/10027632

GENERAL INFORMATION:
TITLE OF INVENTION: OOLYMOOPHISMS in the Human Genome
TITLE OF INVENTION: OOLYMOOPHISMS in the Human Genome
FILE REPERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
FRIOR APPLICATION NUMBER: US 60/18,006
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 28.4%; Score 40; DB 14; Length 11103; Best Local Similarity 53.8%; Pred. No. 0.00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 UUCGAAACCGGGCACUACAAACCAACACACAACACUGAUGAGGA 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 272410
LENGTH: 322
Sequence 23, Application US/10094240 Publication No. US20030082637A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 11103
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ORGANISM: Human
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TYPE: DNA
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GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Pald G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/19,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-01-28
PRIOR PILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1999-01-08
PRIOR FILING DATE: 1999-08-09
PRIOR PRIOR FILING DATE: 1999-08-09
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61.5%; Pred. No. 3.3e-08;
Live 16; Mismatches 9; Indels 0; Gaps
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GENERAL INFORMATION:
APPLICANT Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                   0;
                                                      Query Match 43.4%; Score 61.2; DB 13; Length 818; Best Local Similarity 69.7%; Pred. No. 5.6e-12; Matches 46; Conservative 17; Mismatches 3; Indels 0;
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Best Local Similarity 61.55
Matches 40; Conservative
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US-10-027-632-135532/c
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US-10-027-632-135520
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US-10-027-632-150960
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ORGANISM: Human
                                                             Query Match
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6 UGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUUCGA 65
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GENERAL INFORMATION:
GENERAL INFORMATION:
INFORMATION:
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FITLE OF INVENTION: Dolymorphisms in the Human Genome
FITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REPERBENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/00.07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-10-80
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59.5%; Pred. No. 2.2e-07;
tive 14; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.5%; Score 50; DB 13; Length 817; 58.8%; Pred. No. 5.8e-08; tive 17; Mismatches 11; Indels
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
STOR FILING DATE: 1999-09-28
STOR FILING DATE: 1999-09-28
SOFTWARE: PASTSEQ for Windows Version 4.0
SSOFTWARE: PASTSEQ for Windows Version 4.0
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SOFTWARE: FractSEQ for Windows Version 4.0
SEQ ID NO 146440
LENGTH: 871
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Best Local Similarity 58.8%
Matches 40; Conservative
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364 GACCGGGC 371
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Best Local Similarity
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US-10-027-632-135520
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US-10-027-632-148440
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US-10-027-632-150959
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ORGANISM: Human
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LENGTH: 818
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LENGTH: 818
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REPERENCE: 108827.129
FILE REPERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-12
FRIOR PILING DATE: 2000-07-24
FRIOR PILING DATE: 2000-04-24
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-10-23
FRIOR PILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 46.7%; Score 65.8; DB 13; Length 704; Best Local Similarity 71.8%; Pred. No. 1.2e-13; Matches 51; Conservative 17; Mismatches 3; Indels 0; Gaps
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASKISEQ FOU WINDOWS VERSION 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13961
LENGTH: 704
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US-10-027-632-13960
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US-10-027-632-150959

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33 IGGTTTCCGTAGTGTAGTGGTTATCATGTTCGCCTCACACGCAAAGGTCCCCGGTTCGA 298
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GENERAL INFORMATION:

JITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome

FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/02.04.30

PRIOR PILING DATE: 2002-04.30

PRIOR FILING DATE: 2000-07.12

PRIOR FILING DATE: 2000-07.12

PRIOR FILING DATE: 2000-04.20

PRIOR PLING DATE: 2000-04.20

PRIOR PLING DATE: 2000-03.29

PRIOR PLING DATE: 2000-03.29

PRIOR PLING DATE: 2000-03.29

PRIOR PLING DATE: 2000-02.24

PRIOR PLING DATE: 1999-11.23

PRIOR PLING DATE: 1999-11.23

PRIOR PLING DATE: 1999-10.20

PRIOR PLING DATE: 1999-10.20

PRIOR PLING DATE: 1999-10.20

PRIOR PLING DATE: 1099-10.20

PRIOR PLING DATE: 1099-10.20
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                                                           APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENY APPLICATION NUMBER: US/10/027,632
CURRENY FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 43.4%; Score 61.2; DB 13; Length 818; Best Local Similarity 69.7%; Pred. No. 5.6e-12; Matches 46; Conservative 17; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                PRIOR PELICATION NUMBER: US 60/218,006
PRIOR PELING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 150960, Application US/10027632; GENERAL INFORMATION:
Sequence 150959, Application US/10027632
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                                     GENERAL INFORMATION
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3 CGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGGUU 62
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PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                            Sequence 13959, Application US/10027632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.8<sup>†</sup>
Matches 51; Conservative
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US-10-027-632-13959
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SEQ ID NO 13959
LENGTH: 704
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                                                                                                                                                                         TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a TITLE OF INVENTION: target RNA by recognizing another molecule
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ITTLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REPERBUCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/0430
FRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,383
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1099-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1099-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57.4%; Score 81; DB 11; Length 138; 100.0%; Pred. No. 3e-19; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/974,974
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: JP 2000-313320
PRIOR FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 100 13958
LENGTH: 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13958, Application US/10027632 GENERAL INFORMATION:
                     Sequence 17, Application US/09974974
Publication No. US20030013095A1
GENERAL INFORMATION:
APPLICANT: KAZUNATI TAIRA
APPLICANT: MASSASHINA
APPLICANT: TOMOKO WARASHINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 UUCGAAACCGGGCACUACAAA 81
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Best Local Similarity
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                                                                                                                                                                                                                               FILE REFERENCE:
US-09-974-974-17
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 17
LENGTH: 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: RNA
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3 cenuceunucceuacucuacuceunaucaceunceccuaacaceceaaaecuccceeuu 62
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOINGNOTHISMS in the Human Genome
FILE REPERENCE: 108827.139
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/04/30
FRIOR PILING DATE: 2000-04-20
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-04-20
FRIOR PILING DATE: 2000-03-24
FRIOR PILING DATE: 1900-02-24
FRIOR PILING DATE: 1909-11-23
FRIOR PILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-10-24
FRIOR PILING DATE: 1999-09-10-3
FRIOR PILING DATE: 1999-09-09-09
FRIOR PILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
FRIOR PILING DATE: 1999-08-09
FRIOR PILING DATE: 1999-08-09
FRIOR FILING DATE: 1999-08-09
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PLILING DATE: 2000-07-12
PRIOR PLILING DATE: 2000-07-12
PRIOR PLILING DATE: 2000-07-12
PRIOR PLILING DATE: 2000-04-20
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(without alignments)
2241.006 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                           1632420 seqs, 1213878141 residues
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Listing first 45 summaries
                                               OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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141
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                Sequence:
                                                                                                                                                                                                           Searched:
                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES

		% Ouerv				
Score Matc	Matc	יבן וֹ	Match Length DB	8	D	Description
81 57.	57.	-	88	11	US-09-974-974-5	Sequence 5, Appli
81 57.4	57.4	_	138	ij	US-09-974-974-17	17,
65.8 46.7	46.7	_	704	13	US-10-027-632-13958	П
65.8 46.7	46.7		704	13	US-10-027-632-13959	Sequence 13959, A
65.8 46.7	46.7		704	13	US-10-027-632-13960	Sequence 13960, A
65.8 46.7	46.7		704	13	US-10-027-632-13961	Sequence 13961, A
61.2 43.4	43.4		818	13	US-10-027-632-150959	Sequence 150959,
61.2 43.4	43.4			13	US-10-027-632-150960	Sequence 150960,
50.6 35.9	35.9		603	13	US-10-027-632-135532	Sequence 135532,
50 35.5	35.5		817	13	US-10-027-632-135520	Sequence 135520,
48.4 34.3	34.3			13	US-10-027-632-148440	Sequence 148440,
41.6 29.5	29.5		118067	15	US-10-081-327-32	Sequence 32, Appl
40 28.4	28.4		11103	12	US-10-056-405-23	Sequence 23, Appl
40 28.4	28.4	-	11103	14	US-10-094-240-23	Sequence 23, Appl
39.6 28.1	28.3	_	322	13	US-10-027-632-272410	Sequence 272410,
	27.4		2126	12	US-10-325-107-59	Sequence 59, Appl

RESULT 2

Sequence 100, App Sequence 102, App Sequence 2, Appli Sequence 87, Appl Sequence 10165, A	Sequence 846, App Sequence 3707, Ap Sequence 3777, Ap Sequence 3809, Ap		44	Sequence 308, App Sequence 750, App Sequence 1, Appli Sequence 2210, Ap Sequence 2, Appli Sequence 1, Appli	Sequence 76, Appl Sequence 2, Appli Sequence 199163, Sequence 199164,
9 US-09-842-552-100 9 US-09-842-552-102 11 US-09-884-465A-2 18 US-08-781-986A-87 9 US-08-781-10165	0 US-09-070-927A-846 US-08-781-986A-3707 US-08-781-986A-3777 US-08-781-986A-3809		000	10 US-09-974-300-308 10 US-09-738-626-750 14 US-10-156-761-1 12 US-10-314-455-2210 11 US-09-962-296-2	12 US-10-288-823-76 11 US-09-913-514-2 13 US-10-027-632-199163 13 US-10-027-632-199164
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26.5 26.5 25.7 25.7	25.5 24.7 24.7	22 22 22 22 22 22 24 24 24 25 25 25 25 25 25 25 25 25 25 25 25 25	22222222222222222222222222222222222222	0, (-)	пп
37.4 37.4 37.4 36.2	35 35.4 34.8	34.6 34.2 34.2	34 .2 31 .2 30	200 200 200 200 200 200 200 200 200	28.6 28.6 28.4 28.4
17 18 19 20 21	0000 0000 0000 0000		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

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), OTHER INFORMATION: Description of Artificial Sequence: tRNAVal promoter sequence US-09-974-974-5
                                       Sequence 5, Application US/09974974
Publication No. US20030013095A1
GENERAL INFORMATION:
APPLICANT: Masshi WARASHINA
APPLICANT: Masshi WARASHINA
TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a TITLE OF INVENTION: target RNA by recognizing another molecule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGAAAGGUCCCCGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACCGUUGGUUUCCGUAGUGUAGUGGUUAUCACGUUCGCCUAACACGCGGAAAGGUCCCCGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 57.4%; Score 81; DB 11; Length 88, Best Local Similarity 100.0%; Pred. No. 2.7e-19; Matches 81; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                       FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/974,974
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: JP 2000-313320
PRIOR FILING DATE: 2000-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Pat
SEQ ID NO 5
LENGIH: 88
                  US-09-974-974-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: RNA
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RESULT 1
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